

# HUMAN xiap

```

SEQ ID NO:3      1 gaaagggtggacaagtcctaatttcaagagaagatgacttttaacagtttgaaggatct 60
                  1-----+-----+-----+-----+-----+-----+
SEQ ID NO:4 a    M T F N S F E G S -
                  1-----+-----+-----+-----+-----+-----+
                  61 aaacttggtacctgcagacatcaataaggaagaagaattttagaagagtttaataga 120
                  1-----+-----+-----+-----+-----+-----+
                  K T C V P A D I N K E E F V E E F N R -
                  121 ttaaaaacttttgctaattttccaagtggtagtcctgtttcagcatcaacactggcacga 180
                  1-----+-----+-----+-----+-----+-----+
                  L K T F A N F P S G S P V S A S T L A R -
                  181 gcagggttcttatactggtggaaggagataccgtgcggtgctttagttgtcatgcagct 240
                  1-----+-----+-----+-----+-----+-----+
                  A G F L Y T G E G D T V R C F S C H A A -
                  241 gtagatagatggcaatatggagactcagcagttggaagacacaggaagatcccccaat 300
                  1-----+-----+-----+-----+-----+-----+
                  V D R W Q Y G D S A V G R H R K V S P N -
                  301 tgcagatttatcaacggccttttatcttgaaaaatagtgccacgcagtcctacaattctggt 360
                  1-----+-----+-----+-----+-----+-----+
                  C R F I N G F Y L E N S A T Q S T N S G -

```

Fig. 1A

## HUMAN xiap

```

361  atccagaatggtcagtacaaagttagaaaactatctgggaagcagagatcatttgcctta 420
a    I Q N G Q Y K V E N Y L G S R D H F A L -
361  gacaggccatctgagacacatgcagactatcttttgagaactgggcagggtttagatatata 480
a    D R P S E T H A D Y L L R T G Q V V D I -
361  tcagacaccatataccggaggaaccctgccatgtattgtgaagaagctagattaaagtcc 540
a    S D T I Y P R N P A M Y C E E A R L K S -
361  ttccagaactggccagactatgctcacctaaccccaagagagtagcaagtgctggactc 600
a    F Q N W P D Y A H L T P R E L A S A G L -
361  tactacacaggatttggtgaccaagtgcagtgcttttgtgtgtgggaaactgaaaaaat 660
a    Y Y T G I G D Q V Q C F C C G K L K N -
361  tgggaaccttgatcgtgcctggtcagaacacaggcacactttcctaattgcttctttt 720
a    W E P C D R A W S E H R R H F P N C F F -

```

Fig. 1B

## HUMAN xiap

```

721      gttttggccggaatcttaattcgaagtgaatctgatgctgtgagttctgataggaat 780
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      V L G R N L N I R S E S D A V S S D R N -
      781      ttcccaaatcaacaaatcttccaagaaatcccatccatggcagattatgaagcacggatc 840
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      F P N S T N L P R N P S M A D Y E A R I -
      841      ttacttttgggacatggatatatactcagttaacaaggagcagcttgcaagagctggattt 900
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      F T F G T W I Y S V N K E Q L A R A G F -
      901      tatgcttttaggtgaagggtataaagtaaagtgtcttctcactgtggaggagggtactgat 960
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      Y A L G E G D K V K C F H C G G G L T D -
      961      tggaagcccagtgagacccttgggacaacacatgctaaatggtatccagggtgcaaatat 1020
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      W K P S E D P W E Q H A K W Y P G C K Y -
      1021      ctgttagaacagaagggacaagaatatataaacaatatcttaactcattcacttgag 1080
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      L L E Q K G Q E Y I N N I H L T H S L E -

```

Fig. 1C

## HUMAN xiap

```

1081      gagtgctggtgaactactgagaaaaacaccatcactaactagaagaattgatgatacc 1140
      -----+-----+-----+-----+-----+-----+
a      E C L V R T T E K T P S L T R R I D D T -
      atcttccaaaatcctatggtacaagaagctatacgaaatggggttcagtttcaaggacatt 1200
      -----+-----+-----+-----+-----+-----+
a      I F Q N P M V Q E A I R M G F S F K D I -
      aagaaaataatggaggaaaaaattcagatatctctgggagcaactataaatacacttgaggtt 1260
      -----+-----+-----+-----+-----+-----+
a      K K I M E E K I Q I S G S N Y K S L E V -
      ctggttgcagatctagtgaatgctcagaaagacagtatgcaagatgagtcagtcagact 1320
      -----+-----+-----+-----+-----+-----+
a      L V A D L V N A Q K D S M Q D E S S Q T -
      tcattacagaaagagattagttactgaagagcagctaaggcgccctgcaagaggagaagctt 1380
      -----+-----+-----+-----+-----+-----+
a      S L Q K E I S T E E Q L R R L Q E E K L -
      tgcaaaaatctgtatggatagaaaatttgctatcgtttttgcttccttgtagacatctagtc 1440
      -----+-----+-----+-----+-----+-----+

```

Fig. 1D

## HUMAN xiap

```

a      C K I C M D R N I A I V F V P C G H L V      -
      1441 acttgtaaacaaatgtgctgaagcagttgacaagtgccccatgtgctacacagtcattact 1500
      T C K Q C A E A V D K C P M C Y T V I T      -
      1501 ttcaagcaaaaaatttttatgtcttaactctaatctatatagtaggcattgttatgtgttct 1560
      F K Q K I F M S *      -
      1561 tattaccctgattgaatgtgtgatgtgaactgactttaagtaatcaggattgaattcccat 1620
      tagcatttgctaccaagtaggaaaaaaatgtacatggcagtggttttagttggcaatata 1680
      atctttgaatttcttgatttttcagggtattagctgtattatccattttttttactgtta 1740
      ttttaattgaaccatagactaagaataagaagcatcatactataactgaacacaatgtgt 1800

```

Fig. 1E

attcatagtatactgatttaatttctaagtgtgaagtaataatcatctggattttttat  
 1801 -----+-----+-----+-----+-----+-----+-----+ 1860

1

1861 tttttcagataggcttaacaaatggagcttctgtatataaaatgtggagattagagtta 1920

1

1921 atctcccaatcacataaattgttttgtgtgaaaaggaataaattgtttccatgctggtg 1980

1

1981 gaaagatagagattgttttttagaggttgggttggttggttttaggattctgtccattttct 2040

1

2041 tgtaaggnataaacacgna<sup>+</sup>cntgtcgaaatatn<sup>+</sup>ttgtaaagtga<sup>+</sup>ttgccatt<sup>+</sup>nttg 2100

1

aaagcgtatttaatgatactatcgaggccaacatgtactgcacatggaaagatgtca  
-----+-----+-----+-----+-----+-----+-----+  
2101 2160

Fig. 1F

HUMAN xiaop

2161      nagatatgttaagtgtaaaatgcaagtggcnnnacactatgtatatgtctgagccagatca      2220

॥

2221 aagtatgtatgttnttaatatgcataagaacnanagatttgaaagatatatacaccactg 2280

॥

ttaaattggtttcttcttcggagggggatcgaggggccagaggggttta  
-----+-----+-----+-----+  
2281

ttaaattggtttcttcttcggagggggatcgaggggccagaggggttta  
-----+-----+-----+-----+  
2340

॥

2341 nagggcctttcacttctcnacttttttcattttgttctgttcgnattttttataagtat 2400

॥

gtanacccnaagggttttatgnaactaacatcagtaacctaacccccgtgactatcct  
2401  
2402

၈

gtnctcttcctaggagctgtnntgtttccaccaccaccccttccctctgaacaaatgc  
-----+-----+-----+-----+-----+-----+ 2520

2

ctgagtgcctgggcactttn 2540

10

Fig. 1G

# HUMAN hiap-1

```

SEQ ID NO:5
1      TCCTTGAGATGATCAGTATAGGATTAGGATCTCCATGTTGGAACCTCTAAATGCATAGA 60
-----+-----+-----+-----+-----+-----+-----+
c
61      AATGGAAATAATGGAAATTTTTCATTTTGGCTTTTCAGCCTAGTATTAAACTGATAAAA 120
-----+-----+-----+-----+-----+-----+-----+
c
121     GCAAAGCCATGCACAAAACCTACCTCCCTAGAGAAAGGCTAGTCCCTTTTCTTCCCCATTC 180
-----+-----+-----+-----+-----+-----+-----+
c
181     ATTCATTATGAACATAGTAGAAAACAGCATATTCTTATCAAAATTGATGAAAAGCGCCA 240
-----+-----+-----+-----+-----+-----+-----+
SEQ ID NO:6 c
241     ACACGTTTGAACCTGAAATACGACTTGTGTCATGTGAACTGTACCGAATGTCTACGTATCCA 300
-----+-----+-----+-----+-----+-----+-----+
c
301     T F E L K Y D L S C E L Y R M S T Y S T -
      CTTTCCCTGCTGGGGTTCCTGTCTCAGAAAGGAGTCTTGCTCGTGGTTCATTACA 360
-----+-----+-----+-----+-----+-----+-----+
c
      F P A G V P V S E R S L A R A G F Y Y T -

```

Fig. 2A



## HUMAN hiap-1

```

361      CTGGTGTGAATGACAAGGTCAAATGCTTCTGTGTGGCCTGATGCTGGATAACTGGAAA 420
      -----+-----+-----+-----+-----+-----+-----+
      G V N D K V K C F C C G L M L D N W K R -

421      GAGGAGACAGTCTACTGAAAAGCATATAAAAGTTGTATCCTAGCTGCAGATTCGTTTCAGA 480
      -----+-----+-----+-----+-----+-----+-----+
      G D S P T E K H K K L Y P S C R F V Q S -

481      GTCTAAATTCCGGTTAAACAACCTGGAAAGCTACCTCTCAGCCCTACTTTTCCTTCAGTAA 540
      -----+-----+-----+-----+-----+-----+-----+
      L N S V N N L E A T S Q P T F P S S V T -

541      CACATTCCACACACTCATTACTTCCGGGTACAGAAAACAGTGGATATTCCGGTGGCTCTT 600
      -----+-----+-----+-----+-----+-----+-----+
      H S T H S L L P G T E N S G Y F R G S Y -

601      ATTCAAACTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGAATTTCTGCCTTGA 660
      -----+-----+-----+-----+-----+-----+-----+
      S N S P S N P V N S R A N Q E F S A L M -

661      TGAGAAGTTCCTACCCCTGTCCAATGAATAACGAAAATGCCAGATTACTTACTTTTCAGA 720
      -----+-----+-----+-----+-----+-----+-----+
      R S S Y P C P M N N E N A R L L T F Q T -

```

Fig. 2B

## HUMAN hiap-1

```

721  CATGGCCATTGACTTTTCTGTCGCCAACAGATCTGGCAGCAGGCTTTACTACATAG 780
      W P L T F L S P T D L A R A G F Y Y I G -
841  GACCTGGAGACAGAGTGGCTTGCTTTGCCCTGTGGTGGAAAATTGAGCAATTGGGAACCGA 840
      P G D R V A C F A C G G K L S N W E P K -
901  AGGATAATGCTATGTCAGAACACCTGAGACATTTTCCCAAATGCCCATTTATAGAAAATC 900
      D N A M S E H L R H F P K C P F I E N Q -
961  AGCTTCAAGACACTTCAAGATACACAGTTTCTAACTCTGAGCATGCAGACACATGCAGCCCC 960
      L Q D T S R Y T V S N L S M Q T H A A R -
1021 GCTTTAAACATTCTTTAACTGGCCCTCTAGTGTCTAGTTAATCCTGAGCAGCTTGCAA 1020
      F K T F F N W P S S V L V N P E Q L A S -
      GTGGGGTTTTTATTATGTGGGTAACAGTGATGATGTCAAATGCTTTTGTCTGTATGGTG 1080
      A G F Y Y V G N S D D V K C F C C D G G -

```

Fig. 2C

# HUMAN hiap-1

```

1081 GACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGTTCAACATGCCAAGTGTTCCAA 1140
-----+-----+-----+-----+-----+-----+
C L R C W E S G D D P W V Q H A K W F P R -

1141 GGTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTTTCATCCGTCAAGTTCAAGCCAGTT 1200
-----+-----+-----+-----+-----+-----+
C C E Y L I R I K G Q E F I R Q V Q A S Y -

1201 ACCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCAGGAGATGAAATGCAG 1260
-----+-----+-----+-----+-----+-----+
C P H L L E Q L L S T S D S P G D E N A E -

1261 AGTCATCAATTATCCATTGGAACCTGGAGAAGACCATTTCAGAAGATGCAATCATGATGA 1320
-----+-----+-----+-----+-----+-----+
C S S I I H L E P G E D H S E D A I M M N -

1321 ATACTCCTGTGATTAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCCTGGTAAACAGA 1380
-----+-----+-----+-----+-----+-----+
C T P V I N A A V E M G F S R S L V K Q T -

1381 CAGTTCAGAGAAAATCCTAGCAACTGGAGAGAAATTATAGACTAGTCAATGATCTTGTGT 1440
-----+-----+-----+-----+-----+-----+
C V Q R K I L A T G E N Y R L V N D L V L -

```

Fig. 2D

## HUMAN hiap-1

```

1441 TAGACTTACTCAATGCAGAAGATGAAATAAGGGAAGAGGAGAGAGAAAGCAACTGAGG 1500
-----+-----+-----+-----+-----+-----+
C      D L L N A E D E I R E E R E R A T E E -
1501 AAAAAGAATCAAATGATTATTATTATCCGGAAGAAATAGATGGCACTTTTCAACATT 1560
-----+-----+-----+-----+-----+-----+
C      K E S N D L L L I R K N R M A L F Q H L -
1561 TGACTTGTGTAATCCAATCCTGGATAGTCTACTAAGTCCGGAATTATTAAATGAACAAG 1620
-----+-----+-----+-----+-----+-----+
C      T C V I P I L D S L L T A G I I N E Q E -
1621 AACATGATGTTATTAAACAGAAGACACAGACGCTCTTACAAGCAAGAACTGATTGATA 1680
-----+-----+-----+-----+-----+-----+
C      H D V I K Q K T Q T S L Q A R E L I D T -
1681 CGATTTTAGTAAAGGAAATATTGCAGCCACTGTATTCAAGAACTCTCTGCAAGAAGCTG 1740
-----+-----+-----+-----+-----+-----+
C      I L V K G N I A A T V F R N S L Q E A E -
1741 AAGCTGTGTATATGAGCATTATTGTGCAACAGCACATAAAATATATCCACAGAAG 1800
-----+-----+-----+-----+-----+-----+
C      A V L Y E H L F V Q Q D I K Y I P T E D -

```

Fig. 2E

## HUMAN hiap-1

```

1801  ATGTTTCAGATCTACCAAGTGGAAACAATTGCGGAGACTACCAGAAGAAACATGTA 1860
      V S D L P V E E Q L R R L P E E R T C K -
1861  AAGTGTGTATGGACAAAGAAGTGTCCATAGTGTATTTCCTTGTGGTCATCTAGTAGTAT 1920
      V C M D K E V S I V F I P C G H L V V C -
1921  GCAAAGATTGTGCTCCTTCTTTAAGAAAGTGTCCCTATTGTAGAGTACAATCAAGGGTA 1980
      K D C A P S L R K C P I C R S T I K G T -
1981  CAGTTCGTACATTCTTTTCATGAAGAAGAACCAAAACATCGTCTAAACTTTAGAAATTAAT 2040
      V R T F L S *
2041  TTATTAAATGTATTATAACTTTTAACTTTTATCCTAAATTTGGTTTCCTTAAATTTTATT 2100
      TATTACAACCTCAAAAACAATTGTTTGTGTGAACATATTTATATATATGTATCTAAACCATA 2160

```

Fig. 2F

## HUMAN hiap-1

2161 TGAACATATATTTTGTAGAACTAAGAGAATGATAGGCTTTTGTCTTATGACGAAAAA 2220  
 -----+-----+-----+-----+-----+-----+-----+  
 c -  
 2221 GAGTAGCACTACAAACACAATATTCAATCCAAATTTCAGCATTTATTGAAATTGTAAGTG 2280  
 -----+-----+-----+-----+-----+-----+-----+  
 c -  
 2281 AAGTAAAACTTAAGATATTGAGTTAACCTTTAAGAATTTTAAATATTTTGGCATTGTAC 2340  
 -----+-----+-----+-----+-----+-----+-----+  
 c -  
 2341 TAATACCGGGAACAATGAAGCCAGGTGTGGTGGTAIGTACCTGTAGTCCCAGGCTGAGGCA 2400  
 -----+-----+-----+-----+-----+-----+-----+  
 c -  
 2401 AGAGAACTTACTTGAGCCAGGAGTTTGAATCCATCCTGGGCAGCATACTGAGACCCCTGCC 2460  
 -----+-----+-----+-----+-----+-----+-----+  
 c -  
 2461 TTATAAAACXAAACAGXACCXAAAXCCAAACACCCAGGACACATTTCTGTCTTTTGTGAT 2520  
 -----+-----+-----+-----+-----+-----+-----+  
 c -

Fig. 2G

# HUMAN hiap-1

2521 CAGTGTCTATACATCGAAGGTGTGCATATATGTTGAATCACAATTTTAGGGACATGGTGT 2580

c

2581 TTTTATAAAGAAATTCTGTGAGXAAAAATTTAATAAGCAACCXAAATTACTCTTAAAAAA 2640

c

2641 AAAAAAAAAAAAACTCGAGGGGCGGTACCAAT 2676

c

Fig. 2H

# HUMAN hiap-2

SEQ ID NO:7  
1 TTAGGTTACCTGAAGAGTTACTACAACCCCAAGAGTTGTGTTCTAAGTAGTATCTTGG + 60  
-  
a  
61 TAATTCAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAAAATCCAGTAAAGAAAG + 120  
-  
a  
121 TGTAAGTAAATTCTACATAAGAGTCTATCATTTGTTTGTGGTGGAAATCTTAGTT + 180  
-  
a  
181 CATGTGAAGAAATTTCAATGTGAATGTTTGTAGCTATCAAAACAGTACTGTACCTACTCATG + 240  
-  
a  
241 CACAAACTGCCCTCCCAAGACTTTTCCAGGTCCTCGTATCAAAACATTAAAGAGTATA + 300  
-  
SEQ ID NO:8 a  
301 H K T A S Q R L F P G P S Y Q N I K S I -  
ATGGAAGATAGCAGCATCTTGTGTCAGATTGGACAAACAGCAACAAACAAATGAAGTAT + 360  
-  
a  
M E D S T I L S D W T N S N K Q K M K Y -

Fig. 3A



## HUMAN hiap-2

```

361      GACTTTTCTGTGAACCTCTACAGAATGCTACATATTCAACTTCCCCCGGGGTGCCT 420
      -----+-----+-----+-----+-----+-----+
a      D F S C E L Y R M S T Y S T F P A G V P -

421      GTCTCAGAAAGGAGTCTTGCTCGTGGTGGTTTATTATATACTGGTGTGAATGACAAGTC 480
      -----+-----+-----+-----+-----+-----+
a      V S E R S L A R A G F Y Y T G V N D K V -

481      AAATGCTTCTGTGGCCTGATGCTGGATAACTGGAAC TAGGAGACAGTCCTATTCAA 540
      -----+-----+-----+-----+-----+-----+
a      K C F C C G L M L D N W K L G D S P I Q -

541      AAGCATAACAGCTATATCCTAGCTGTAGCTTTATTTCAGAATCTGGTTTCAGCTAGTCTG 600
      -----+-----+-----+-----+-----+-----+
a      K H K Q L Y P S C S F I Q N L V S A S L -

601      GGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTGGCACATTATCTCTCCC 660
      -----+-----+-----+-----+-----+-----+
a      G S T S K N T S P M R N S F A H S L S P -

661      ACCTTGGAACATAGTACTTGTTCAGTGGTTCTTACTCCAGCCTTCCTCCAAACCCCTCTT 720
      -----+-----+-----+-----+-----+-----+
a      T L E H S S L F S G S Y S S L P P N P L -

```

Fig. 3B

## HUMAN hiap-2

```

721  AATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAATG 780
a   N S R A V E D I S S S R T N P Y S Y A M -
781  AGTACTGAAGAAGCCAGATTCTTCTTACCTACCATATGTGGCCATTAACTTTTGTCCACCA 840
a   S T E E A R F L T Y H M W P L T F L S P -
841  TCAGAAATTGGCAAGAGCTGGTTTTATTATATAGGACCTGGAGATAGGGTAGCCTGCTTT 900
a   S E L A R A G F Y Y I G P G D R V A C F -
901  GCCTGTGGTGGGAAGCTCAGTAACTGGGAACCAAGGATGATGCTATGTCAGAACACCCGG 960
a   A C G G K L S N W E P K D D A M S E H R -
961  AGGCATTTCCCAACTGTCCATTTTGGAAAATTCTCTAGAAACTCTGAGGTTAGCATT 1020
a   R H F P N C P F L E N S L E T L R F S I -
1021 TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTATGTACTGGCCATCT 1080
a   S N L S M Q T H A A R M R T F M Y W P S -

```

Fig. 3C

## HUMAN hiap-2

```

1081 AGTGTTCAGTTCAGCCTGAGCAGCTTGCAAGTCTGGTGTGTTTATTATGTGGTTCGCAAT 1140
a   S V P V Q P E Q L A S A G F Y Y V G R N -
1141 GATGATGTCAAATGCTTTGGTTGTGATGGTGGCTTGAGGTGTGGGAATCTGGAGATGAT 1200
a   D D V K C F G C D G G L R C W E S G D D -
1201 CCATGGGTAGAAATGCCAAGTGGTTCCAAGGTGTGAGTCTTGTATACGAATGAAAGGC 1260
a   P W V E H A K W F P R C E F L I R M K G -
1261 CAAGAGTTTGTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGCTGTGTGCA 1320
a   Q E F V D E I Q G R Y P H L L E Q L L S -
1321 ACTTCAGATACCACTGGAGAAGAAAATGCTGACCCCAATATTATCTTTGGACCTGGA 1380
a   T S D T T G E E N A D P P I I H F G P G -
1381 GAAAGTTCTTCAGAAGATGCTGTGATGATGAATACACCTGTGGTTAAATCTGCCCTTGAA 1440
a   E S S S E D A V M M N T P V V K S A L E -

```

Fig. 3D

## HUMAN hiap-2

1441	ATGGGCTTTAATAGAGACCTGGTGAACAACAGTTCTAAGTAAATCCTGCAACTGGA	1500
a	M G F N R D L V K Q T V L S K I L T T G	-
1501	GAGAACTATAAACAGTTAATGATATTGTGTCAGCACTTCTTAATGCTGAAGATGAAAAA	1560
a	E N Y K T V N D I V S A L L N A E D E K	-
1561	AGAGAAGAGGAGGAGGAAAAACAAGCTGAAGAAATGGCATCAGATGATTTGTCATTAATT	1620
a	R E E E K E K Q A E E M A S D D L S L I	-
1621	CGGAAGAACAGAAATGGCTCTCTTTCAACAATTGACATGTGTGCTTCCTATCCTGGATAAT	1680
a	R K N R M A L F Q Q L T C V L P I L D N	-
1681	CTTTTAAAGGCCAATGTAATTAATAAACAGGAACATGATATTATTAAACAAAAACACAG	1740
a	L L K A N V I N K Q E H D I I K Q K T Q	-
1741	ATACCTTTACAAGCGAGAGAACTGATTGATACCATTGGGTTAAGGAAATGCTGCGGCC	1800
a	I P L Q A R E L I D T I W V K G N A A A	-

Fig. 3E

## HUMAN hiap-2

```

1801 AACATCTTCAAAACTGTCTAAAGAAATTGACTCTACATTGTATAAGAACTTATTGTG 1860
a   N I F K N C L K E I D S T L Y K N L F V -
    GATAAGAAATATGAAGTATATTCCAACAGAAGATGTTTCAGGCTGTCTCACTGGAAGAACAA 1920
1861 -----+-----+-----+-----+-----+-----+
a   D K N M K Y I P T E D V S G L S L E E Q -
    TTGAGGAGGTTGCAAGAAGAACTTGTAAGTGTGTATGGACAAAGAAGTTTCTGT 1980
1921 -----+-----+-----+-----+-----+-----+
a   L R R L Q E E R T C K V C M D K E V S V -
    GTATTTATTCCTTGTGGTCATCTGGTAGTATGCCAGGAATGTCCCTTCTCTAAGAAA 2040
1981 -----+-----+-----+-----+-----+-----+
a   V F I P C G H L V V C Q E C A P S L R K -
    TGCCCTATTGCAGGGGTATAATCAAGGGTACTGTTCGTACATTTCTCTCTTAAAGAAA 2100
2041 -----+-----+-----+-----+-----+-----+
a   C P I C R G I I K G T V R T F L S * -
    ATAGTCTATATTTAACCTGCATAAAAGGCTTTAAATATTGTTGAACACTTGAAGCC 2160
2101 -----+-----+-----+-----+-----+-----+
a

```

Fig. 3F

## HUMAN hiap-2

```

2161 ATCTAAAGTAAAAGGGAATTATGAGTTTTTCAATTAGTAACATTCATGTTCTAGTCTGC 2220
      -
a
2221 TTTGGTACTAATAATCTTGTCTGAAAAGATGGTATCATATATTAACTTAATCTGTT 2280
      -
a
2281 TATTTACAAGGAAGATTATGTTTGTGGAACATATATTAGTATGTATGTGTACCTAAGGG 2340
      -
a
2341 AGTAGCGTCXCTGCTTGTATGCATCATTTTCAGGAGTTACTGGATTGTGTTCTTTCAG 2400
      -
a
2401 AAAGCTTTGAAXACTAAATTATAGTGTAGAAAAGAACTGGAAACCAGGAACCTCTGGAGTT 2460
      -
a
2461 CATCAGAGTTATGGTGCCGAATTGTCTTTTGGTGCTTTTTCACCTTGTGTTTAAATAAGGA 2520
      -
a
2521 TTTTCTCTTATTTCTCCCCCTAGTTTGTGTGAGAAACATCTCAATAAAGTGCTTTAAAG 2580
      -
a

```

Fig. 3G

## MOUSE xiap

```

SEQ ID NO:9          1      60
GACACTCTGCTGGCGGGCGCCCTCCTCCGGGACCTCCCTCGGGAACCGTCGCCC
-----+-----+-----+-----+-----+-----+
a

61      120
GCGGCGCTTAGGACTGGAGTGCTTGGCGCGAAAGGTGGACAAGTCCTATTTCCA
-----+-----+-----+-----+-----+-----+
a

121      180
GAGAAGATGACTTTTAACAGTTTGAAGGAAGTAACTTTTGTAAGTGCAGACCAAT
-----+-----+-----+-----+-----+-----+
M T F N S F E G T R T F V L A D T N

181      240
AAGGATGAAGAAATTTGTAGAAGAGTTTAATAGATTAAAAACATTGTCTAACTTCCCAAGT
-----+-----+-----+-----+-----+-----+
K D E E F V E E F N R L K T F A N F P S

241      300
AGTAGTCCTGTTTCAGCATCAACATTGGCGCGAGCTGGGTTTCTTATACCGTGAAGGA
-----+-----+-----+-----+-----+-----+
a

301      360
GACACCGTGCAATGTTTCAGTTGTGTCATGCGGCAATAGATGGCAGTATGGAGACTCA
-----+-----+-----+-----+-----+-----+
a

D T V Q C F S C H A A I D R W Q Y G D S

```

Fig. 4A

## MOUSE xiap

```

361      GCTGTTGGAAGACACAGGAGAATATCCCCAAATTGCAGATTATCAATGGTTTATTTT 420
      -----+-----+-----+-----+-----+-----+-----+
a      A V G R H R R I S P N C R F I N G F Y F -
      -----+-----+-----+-----+-----+-----+-----+
421      GAAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAATGGCCAGTACAAATCTGAA 480
      -----+-----+-----+-----+-----+-----+-----+
a      E N G A A Q S T N P G I Q N G Q Y K S E -
      -----+-----+-----+-----+-----+-----+-----+
481      AACTGTGTGGAAATAGAAATCCTTTTGCCCTGACAGGCCACCTGAGACTCATGCTGAT 540
      -----+-----+-----+-----+-----+-----+-----+
a      N C V G N R N P F A P D R P P E T H A D -
      -----+-----+-----+-----+-----+-----+-----+
541      TATCTCTGAGAACTGGACAGGTTGTAGATATTCAGACACCATATACCCGAGGAACCT 600
      -----+-----+-----+-----+-----+-----+-----+
a      Y L L R T G Q V V D I S D T I Y P R N P -
      -----+-----+-----+-----+-----+-----+-----+
601      GCCATGTGTAGTGAAGCCAGATTGAAGTCATTCAGAACTGGCCGACTATGCTCAT 660
      -----+-----+-----+-----+-----+-----+-----+
a      A M C S E E A R L K S F Q N W P D Y A H -
      -----+-----+-----+-----+-----+-----+-----+
661      TTAACCCACAGAGTTAGCTAGTGTGGCTCTACTACACAGGGCTGATCAAGTG 720
      -----+-----+-----+-----+-----+-----+-----+
a      L T P R E L A S A G L Y Y T G A D D Q V -

```

Fig. 4B



## MOUSE xiap

```

721 CAATGCTTTTGTGGGGAAAACCTGAAAAATTGGGAACCCCTGTGATCGTGCCCTGGTCA 780
-----+-----+-----+-----+-----+-----+
a   Q C F C C G G K L K N W E P C D R A W S -
781 GAACACAGGAGACACTTCCCAATGCTTTTGTGTTTGGCCGGAACGTTAATGTTTCA 840
-----+-----+-----+-----+-----+-----+
a   E H R R H F P N C F F V L G R N V N V R -
841 AGTGAATCTGGTGTGAGTTCTGTAGGAATTCCCAAATTCAACAACTCTCCAAGAAAT 900
-----+-----+-----+-----+-----+-----+
a   S E S G V S S D R N F P N S T N S P R N -
901 CCAGCCATGGCAGAAATATGAAGCACGGATCGTTACTTTTGGAAACATGGATATACTCAGTT 960
-----+-----+-----+-----+-----+-----+
a   P A M A E Y E A R I V T F G T W I Y S V -
961 AACAAAGGAGCAGCTTGCAAGAGCTGGATTATTATGCTTTAGGTGAAGCGGATAAAGTGAAG 1020
-----+-----+-----+-----+-----+-----+
a   N K E Q L A R A G F Y A L G E G D K V K -
1021 TGCTTCCACTGTGGAGGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAG 1080
-----+-----+-----+-----+-----+-----+
a   C F H C G G G L T D W K P S E D P W D Q -

```

Fig. 4C

## MOUSE xiap

```

1081 CATGCTAAGTGCTACCCAGGTGCAAAATACCTATTGGATGAGAAGGGCAAGATATATA 1140
a   H A K C Y P G C K Y L L D E K G Q E Y I -
1141 AATAATATTCAATTAAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAAAACA 1200
a   N N I H L T H P L E E S L G R T A E K T -
1201 CCACCGCTAACTAAAAATCGATGATACCATCTTCCAGAATCCTATGGTGCAAGAAGCT 1260
a   P P L T K K I D D T I F Q N P M V Q E A -
1261 ATACGAATGGGATTAGCTTCAAGGACCTTAAGAAAAACAATGGAAGAAAAAATCCAAACA 1320
a   I R M G F S F K D L K K T M E E K I Q T -
1321 TCCGGAGCAGCTATCTACTTGAGGTCTTGATTCAGAGATCTTGTGAGTGTCTCAGAAA 1380
a   S G S S Y L S L E V L I A D L V S A Q K -
1381 GATAATACGGAGGATGAGTCAAGTCAAACTTCATTGCAGAAAGACATTAGTACTGAAGAG 1440
a   D N T E D E S S Q T S L Q K D I S T E E -

```

Fig. 4D

## MOUSE xiap

```

1441 CAGCTAAGGCGCCTACAAGAGGAGAAAGCTTTCCAAATCTGTATGGATAGAAATATTGCT 1500
-----+-----+-----+-----+-----+-----+-----+
a   Q L R R L Q E E K L S K I C M D R N I A -
    ATCGTTTTTTTTCCTTGTGGACATCTGGCCACTTGTAAACAGTGTGCAGAACGAGTTGAC 1560
-----+-----+-----+-----+-----+-----+-----+
a   I V F F P C G H L A T C K Q C A E A V D -
    AAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAATTTTATGCTTAGTGG 1620
-----+-----+-----+-----+-----+-----+-----+
a   K C P M C Y T V I T F N Q K I F M S * -
    GGCACCACATGTTATGTTCTTCTTGTCTCTAATTGAATGTGTAATGGGAGCGAACTTTAAG 1680
-----+-----+-----+-----+-----+-----+-----+
a   TAATCCTGCATTTCATTCCATTAGCATCCCTGCTGTTTCCAAATGGAGACCAATGCTAAC 1740
-----+-----+-----+-----+-----+-----+-----+
a   AGCACTGTTTCCGTCCTAAACATTCAATTCTCGGATCTTTCGAGTTATCAGCTGTATCATT 1800
-----+-----+-----+-----+-----+-----+-----+
a

```

Fig. 4E

## MOUSE xiap

```

1801 TAGCCAGTGTTTACTCGATTGAACCTTAGACAGAGAAGCATTTTATAGCTTTTCACAT 1860
      -
a
1861 GTATATTGGTAGTACACTGACTTGATTCTATATGTAAGTGAATTCATCACCTGCATGTT 1920
      -
a
1921 TCATGCCCTTTGCATAAGCTTAACAAATGGAGTGTCTGTATAAGCATGGAGATGTGATG 1980
      -
a
1981 GAATCTGCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAGAAGCTGCCCCACGCTG 2040
      -
a
2041 CTGGGAGGATAAAGATTGTTTATAGATGCTCACTTCTGTGTTTATAGGATTCTGCCCATTTA 2100

```

Fig. 4F

## M-hiap-1

```

SEQ ID NO:39      1  GAATTCGGGAGACCTACACCCCGGAGATCAGAGGTCAATGCTGGCGTTCAGAGCCTAG  60
  -----+-----+-----+-----+-----+-----+-----+-----+
 61  GAAGTGGGCTGCGGTATCAGCCTAGCAGTAAACCGACCAGAGCCATGCACAAACTAC  120
  -----+-----+-----+-----+-----+-----+-----+-----+
121  ATCCCCAGAGAAAGACTTGTCCCTTCCCTCCCTGTCACTCTCACCATGAACATGGTTCAA  180
  -----+-----+-----+-----+-----+-----+-----+-----+
                               M N M V Q -
                               -
181  GACAGCGCCTTTCTAGCCAAGCTGATGAAGAGTGTGACACCTTTGAGTTGAAGTATGAC  240
  -----+-----+-----+-----+-----+-----+-----+-----+
  D S A F L A K L M K S A D T F E L K Y D -
241  TTTTCCTGTGAGCTGTACCGATTGTCCACGTATTCAGCTTTTCCCAGGGGAGTTCCTGTG  300
  -----+-----+-----+-----+-----+-----+-----+-----+
  F S C E L Y R L S T Y S A F D R G V P V -
301  TCAGAAAGGAGTCTGGCTCGTGGCTTTTACTACACTGGTGCCTCAATGACAAGGTCAAG  360
  -----+-----+-----+-----+-----+-----+-----+-----+
  S E R S L A R A G F Y Y T G A N D K V K -
361  TGCTTCTGTGGCCTGATGCTAGACAACTGGAAACAAGGGGACAGTCCCATGGAGAAG  420
  -----+-----+-----+-----+-----+-----+-----+-----+
  C F C C G L M L D N W K Q G D S P M E K -

```

Fig. 5A

## M-hiap-1

```

421  CACAGAAAGTTGTACCCAGCTGCAACTTTGTACAGACTTTGAATCCAGCCAACAGTCTG
      H R K L Y P S C N F V Q T L N P A N S L -
      480

481  GAAGCTAGTCCTCGGCCTTCTCTCTCCACGGGATGAGCACCATGCTTGTGAGCTTT
      E A S P R P S L P S T A M S T M P L S F -
      540

541  GCAAGTCTGAGAATACTGGCTATTTCAGTGGCTCTTACTCGAGCTTTCCTCAGACCCT
      A S S E N T G Y F S G S Y S S F P S D P -
      600

601  GTGAACTTCCGAGCAAATCAAGATTGTCTGCTTTGAGCACAAAGTCCCTACCACCTTGCA
      V N F R A N Q D C P A L S T S P Y H F A -
      660

661  ATGAACACAGAGAAGGCCAGATTACTCACCTATGAACATGGCCATTGTCTTCTGTCA
      M N T E K A R L L T Y E T W P L S F L S -
      720

721  CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGGACCTGGAGATAGAGTGGCCTGC
      P A K L A K A G F Y Y I G P G D R V A C -
      780

```

Fig. 5B

# M-hiap-1

```

781  TTTGCGTGGGAAACTGAGCAACTGGGAACGTAAGGATGATGCTATGTCAGAGCAC 840
      F A C D G K L S N W E R K D D A M S E H -
      -----+-----+-----+-----+-----+-----+-----+
841  CAGAGGCATTTCCCCAGCTGTCCGTTCTTALLKACTTGGGTCAGTCTGCTTCGAGATAC 900
      Q R H F P S C P F L K D L G Q S A S R Y -
      -----+-----+-----+-----+-----+-----+-----+
901  ACTGTCTCTAACCTGAGCATGCAGACACACGACGCCCGTATTAGAACATTCTCTAACTGG 960
      T V S N L S M Q T H A A R I R T F S N W -
      -----+-----+-----+-----+-----+-----+-----+
961  CCTTCTAGTGCACTAGTTCAATTCACAGGAACCTTGCAAGTGGGGCTTTATTATACAGGA 1020
      P S S A L V H S Q E L A S A G F Y Y T G -
      -----+-----+-----+-----+-----+-----+-----+
1021 CACAGTGATGATCAAGTGTATTATGCTGTGATGGTGGCTGAGGTGCTGGGAATCTGGA 1080
      H S D D V K C L C C D G G L R C W E S G -
      -----+-----+-----+-----+-----+-----+-----+
1081 GATGACCCCTGGGTGGAACATGCCAAGTGGTTTCCAAAGGTGTGAGTACTTGCTCAGAATC 1140
      D D P W V E H A K W F P R C E Y L L R I -
      -----+-----+-----+-----+-----+-----+-----+
1141 AAAGGCCAAGAAATTTGTCAGCCCAAGTTCAGCTGGCTATCCTCATCTACTTGAGCAGCTA 1200
      K G Q E F V S Q V Q A G Y P H L L E Q L -
      -----+-----+-----+-----+-----+-----+-----+

```

Fig. 5C

## M-hiap-1

```

1201 TTATCTACGTCACTCCCCAGAAGATGAGAATGCAGACGCAGCAATCGTGCAATTTGGC 1260
      L S T S D S P E D E N A D A A I V H F G -
1261 CCTGGAGAAAGTTCGGAAGATGTCGTCAATGATGAGCACGCCCTGTGGTTAAAGCAGCCCTTG
      P G E S S E D V V M M S T P V V K A A L -
1320
1321 GAAATGGGCTTCAGTAGGAGCCCTGGTGAGACAGACGGTTCAGTGGCAGATCCTGGCCACT 1380
      E M G E S R S L V R Q T V Q W Q I L A T -
1381 GGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATGCAGAAGACGAG 1440
      G E N Y R T V S D L V I G L L D A E D E -
1441 ATGAGAGAGGAGCAGATGGAGCAGCGCGCCGAGGAGGAGTCAATGATCTAGCACTA 1500
      M R E E Q M E Q A A E E E E S D D L A L -
1501 ATCCGGAAGAACAATGGTGCTTTTCCAACATTGACGTGTGTGACACCAATGCTGTAT 1560
      I R K N K M V L F Q Q H L T C V T P M L Y -

```

Fig. 5D



## M-hiap-1

```

1561 TGCCTCCTAAGTGCAAGGGCCATCACTGAACAGGAGTGCAATGCTGTGAAACAGAAACCA
      C L L S A R A I T E Q E C N A V K Q K P - 1620
1621 CACACCTTACAAGCAAGCACACTGATTGATACTGTGTTAGCAAAAGGAAACACTGCAGCA
      H T L Q A S T L I D T V L A K G N T A A - 1680
1681 ACCTCATTCAGAAACTCCCTTCGGGAAATTGACCCCTGCGTTATACAGAGATATTTGTG
      T S F R N S L R E I D P A L Y R D I F V - 1740
1741 CAACAGGACATTAGGAGTCTTCCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG
      Q Q D I R S L P T D D I A A L P M E E Q - 1800
1801 TTGGGGCCCTCCCGGAGGACAGAAATGTGTAAGTGTATGGACCGAGAGGTATCCATC
      L R P L P E D R M C K V C M D R E V S I - 1860
1861 GTGTTCAATCCCTGTGGCCATCTGGTCGTGTGCAAGACTGCGCTCCCTCTCTGAGGAAG
      V F I P C G H L V V C K D C A P S L R K - 1920

```

Fig. 5E

## M-hiap-1

```

1921 TGTCCCATCTGTAGAGGGACCATCAAGGGCACAGTGGGCACATTTCTCTCCTGAACAAGA 1980
      C P I C R G T I K G T V R T F L S * -
1981 CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACCTGTCACTCCAGTTCCCAT 2040
      TCGGAACCTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACKCACAAATATAAACAT 2100
2041 GAAAAACCTTTTGTCTGAAGTCAAGAAATGAATGAATTACTTATATAATAATTTAATTGGT 2160
2101 TTCCCTTAAAGTGCTATTGTTCCTCCAACTCAGAAAAATTGTTTCTGTAAACATATTACA 2220
2161 TACTACCTGCATCTAAAGTATTTCATATATTCATATATTCAGATGTCATGAGAGGGGTTT 2280
2221 TGTTCTTGTTCCCTGAAAAGCTGGTTTATCATCTGATCAGCATATATACTGGCGCAACGGGCAG 2340
2281 GGCTAGAATCCATGAACCAAGCTGCAAGATCTCACGCTAAATAAGGCGGAAAGATTGG 2400
2341 AGAAACGAAAGGAAATCTTTCTGTCCCAATGTATACCTTCAGACTAATGACCTCTTCC 2460
2401 TATCAAGCCTTCTA
2461 -----+----- 2474

```

Fig. 5F

# M-hiap-2

```

SEQ ID NO:41
1  CTGTGGTGAGATCTATTGTCCAAGTGGTGAGAACTTCATCTGGAAGTTTAAGCGGTCA
60  GAAATACTATTACTACTCATGGACAKRACTGTCTCCAGAGACTCGCCCAAGGTACCTTA
61  CACCCRAAAACTTAAACGTATAATGGAGAAGAGACACAATCTTGTCAAATTGGACAAAGGA
121 -----+-----+-----+-----+-----+-----+
180 M E K S T I L S N W T K E -
SEQ ID NO:42
181 GAGCGAAGAAAAATGAAGTTTGACTTTTCGTGTGAACCTCTACCGAATGTCTACATATTC
240 S E E K M K F D F S C E L Y R M S T Y S -
241 AGCTTTTCCAGGGGAGTTCCTGTCTCAGAGAGGAGTCTGGCTCGTGGCTTTTATTA
300 A F P R G V P V S E R S L A R A G F Y Y -
301 TACAGGTGTGAATGACAAAGTCAAGTGCTTCTGTGTGGCCCTGATGTGGATAACTGGAA
360 T G V N D K V K C F C C G L M L D N W K -
361 ACAAGGGGACAGTCCCTGTGTTGAAAAGCACAGACAGTCTATCCAGCTGCAGCTTGTACA
420 Q G D S P V E K H R Q F Y P S C S F V Q -

```

Fig. 6A

## M-hiap-2

```

421  GACTCTGCTTTCAGCCAGTCTGCAGTCTCCATCTAAGAAATATGTCTCTGTGAAAAGTAG
      T L L S A S L Q S P S K N M S P V K S R -
480  -----+-----+-----+-----+-----+-----+-----+

481  ATTTGCACATTCTGTCACCTCTGGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC
      F A H S S P L E R G G I H S N L C S S P -
540  -----+-----+-----+-----+-----+-----+-----+

541  TCTTAATTCTAGAGCAGTGGGAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT
      L N S R A V E D F S S R M D P C S Y A M -
600  -----+-----+-----+-----+-----+-----+-----+

601  GAGTACAGAAGAGGCCAGATTCTTACTTACAGTATGTGGCCTTTAAGTTTCTGTCAACC
      S T E E A R F L T Y S M W P L S F L S P -
660  -----+-----+-----+-----+-----+-----+-----+

661  AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGCCCTGGAGACAGGGTGGCCTGTTT
      A E L A R A G F Y Y I G P G D R V A C F -
720  -----+-----+-----+-----+-----+-----+-----+

721  TGCCTGTGTGGAAACTGAGCAACTGGGAACCAAGGATTATGCTATGTCAGAGCACCG
      A C G G K L S N W E P K D Y A M S E H R -
780  -----+-----+-----+-----+-----+-----+-----+

```

Fig. 6B

## M-hiap-2

```

781  CAGACATTTCCCACTGTCCATTCTCTGGAAAATACTTCAGAAACACAGAGGTTAGTAT 840
      R H F P H C P F L E N T S E T Q R F S I -
841  ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACC 900
      S N L S M Q T H S A R L R T F L Y W P P -
901  TAGTGTTCCTGTTCAAGCCGAGCAGCTTGCAAGTGTGGATTCTATTACGTGGATCGCRA 960
      S V P V Q P E Q L A S A G F Y Y V D R N -
961  TGATGATGTCAAGTGCCCTTTGTTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGA 1020
      D D V K C L C C D G G L R C W E P G D D -
1021 CCCCTGGATAGAACACGCCAAATGGTTTCCAAAGTGTGAGTCTTGATACGGATGAAGGG 1080
      P W I E H A K W F P R C E F L I R M K G -
1081 TCAGGAGTTTGTGATGAGATTCAAGCTAGATATCCTCACTCTTGAGCAGCTGTGTGC 1140
      Q E F V D E I Q A R Y P H L L E Q L L S -

```

Fig. 6C

## M-hiap-2

```

1141 CACTTCAGACACCCAGGAGAAGAAATGCTGACCCCTACAGAGACAGTGGTGCAATTTGG
-----+-----+-----+-----+-----+-----+
      T S D T P G E E N A D P T E T V V H F G - 1200

1201 CCCTGGAGAAAGTTCGAAAGATGTCGTCAATGATGAGCACGCCCTGTGGTTAAAGCAGCCTT
-----+-----+-----+-----+-----+-----+
      P G E S S K D V V M M S T P V V K A A L - 1260

1261 GGAATGGGCTTCAGTAGGAGCCCTGGTGAGACAGACGGTTCAGCGGCAGATCCTGGCCAC
-----+-----+-----+-----+-----+-----+
      E M G F S R S L V R Q T V Q R Q I L A T - 1320

1321 TGGTGAGAACTACAGGACCGTCAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGA
-----+-----+-----+-----+-----+-----+
      G E N Y R T V N D I V S V L L N A E D E - 1380

1381 GAGAGAGAGAGGAGAGGAAAGACAGACTGAAGAGATGGCATCAGGTGACTTATCACT
-----+-----+-----+-----+-----+-----+
      R R E E E K E R Q T E E M A S G D L S L - 1440

1441 GATTCGGAAGAATAGAAATGGCCCTCTTTCAACAGTTGACACATGTCCTTCCTATCCTGGA
-----+-----+-----+-----+-----+-----+
      I R K N R M A L E Q Q L T H V L P I L D - 1500

```

Fig. 6D

## M-hiap-2

```

1501 TAATCTTCTTGAGGCCAGTGTAATTACAAAACAGGAACATGATATTATTAGACAGAAAC
      N L L E A S V I T K Q E H D I I R Q K T - 1560
1561 ACAGATACCCCTTACAAGCAAGAGAGCTTATTGACACCGTTTGTAGTCAAGGGAATGCTGC
      Q I P L Q A R E L I D T V L V K G N A A - 1620
1621 AGCCAACATCTTCAAAAACCTCTCTGAAGGGAATTGACTCCACGTTATATGAAAACCTTATT
      A N I F K N S L K G I D S T L Y E N L F - 1680
1681 TGTGAAAAGAATATGAAGTATATCCACAGAAACGTTTCAGGCTTGTTCATTGGAAGA
      V E K N M K Y I P T E D V S G L S L E E - 1740
1741 GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAAAGTGTGTATGGACAGAGAGTTTC
      Q L R R L Q E E R T C K V C M D R E V S - 1800
1801 TATTGTGTTTCATTCGTTGGTCATCTAGTAGTCTGCCAGGAATGTGCCCTTCTCTAAG
      I V F I P C G H L V V C Q E C A P S L R - 1860

```

Fig. 6E

## M-hiap-2

```

1861 GAAGTGCCCATCTGCAGGGGACAAATCAAGGGGACTGTGCGCACATTTCTCTCATGAGT 1920
      K C P I C R G T I K G T V R T F L S *
1921 GAAGAAATGGTCTGAAAGTATTGTTGGACATCAGAAGCTGTCAGAAACAAAGAATGAACCTAC 1980
      TGATTTCAAGCTCTTCAGCAGGACATTCTACTCTCTTTCAAGATTAGTAATCTTGCTTTAT
1981 -----+-----+-----+-----+-----+-----+-----+ 2040
      GAAGGTAGCATTTGTATATTAAAGCTTAGTCTGTTGCAAGGGAAGGCTATGCTGTTGAG
2041 -----+-----+-----+-----+-----+-----+-----+ 2100
      CTACAGGACTGTGTCTGTTCCAGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGA
2101 -----+-----+-----+-----+-----+-----+-----+ 2160
      CTTCTTGGGATTGGAATTGSGGAAAGCTTTGGAATCCAGTGATGTGGAGCTCAGAAA
2161 -----+-----+-----+-----+-----+-----+-----+ 2220
      TCCTGGAACCAAGTACTCTGGTACTCAGTAGATAGGGTACCCTGTACTTCTTGGTGCTTT
2221 -----+-----+-----+-----+-----+-----+-----+ 2280
      TCCAGTCTGGGAAATAAGGAGGAATCTGCTGCTGTGTAATAATTGCTGGATGTGAGAAAT
2281 -----+-----+-----+-----+-----+-----+-----+ 2340
      AGATGAAAGTGTTCGGGGTGGGGCGTGCAATCAGTGATGTGTGCAGGGATGTATGCAG
2341 -----+-----+-----+-----+-----+-----+-----+ 2400
      GCCAAACACTGTGTAG
2401 -----+-----+-----+-----+-----+-----+-----+

```

Fig. 6F



# Alignment of BIR (Baculoviral IAP Repeats) Domains

Baculovirus  
Cp\_iap  
Op\_iap  
Human  
xiap  
hiap1, hiap2  
Mouse  
m-xiap  
Insect  
diap

Cydia pomonella  
Orgyia pseudotsugata

IAP on X chromosome  
two different human IAP genes

mouse homologue of human xiap gene

Drosophila IAP gene, not clearly a homologue of xiap or hiap

Fig. 7

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence.

SEQ ID NO:11	Op_iap-1	kaarLgTYtn	WPvqf.l	leps	rMAasGFYYL	GrgDeVrCaf	CkveitnWvr	gDdpetdHkr	wapqCpFV	68
SEQ ID NO:14	Cp_iap-1	eevRlnTFek	WPvsf.l	lspe	tMAknGFYYL	GrgDeVrCaf	CkveimrWke	gEdpaadHkk	wapqCpFV	
SEQ ID NO:15	diap-2	eanRLvTFkd	WPnnpn.i	lPq	aLAKAGFYI	nrlDhVkcVw	CngviakWek	nDnafeeHkr	ffpqCprV	
SEQ ID NO:16	m-xiap-1	efnRLkTFan	FPsspsvas	tLARAGFLYt	GegDtVqCFs	ChaaidrWqy	gDSavgrHrr	ispnCrFI		
SEQ ID NO:17	xiap-1	efnRLkTFan	FPsgspvas	tLARAGFLYt	GegDtVrCFs	ChaaavdrWqy	gDSavgrHrk	vspnCrFI		
SEQ ID NO:18	hiap1-1	elyRMstYst	FPagvpvser	sLARAGFYt	GvndkVkcFC	CglmldnWkl	gDSptekHkk	lypsCrFV		
SEQ ID NO:19	hiap2-1	elyRMstYst	FPagvpvser	sLARAGFYt	GvndkVkcFC	CglmldnWkl	gDspiqkHkq	lypsCsFI		
SEQ ID NO:20	m-xiap-2	eearLksFqn	WPdyahltptr	eLASAGLLYt	GadDqVqCFc	CggklknWep	cDrawseHrr	hfpnCcFV		
SEQ ID NO:21	xiap-2	eearLksFqn	WPdyahltptr	eLASAGLLYt	GadDqVqCFc	CggklknWep	cDrawseHrr	hfpnCcFV		
SEQ ID NO:22	hiap1-2	enaRLlTFqt	WP.lflspt	dLARAGFYI	GpgDrVaCfa	CggklknWep	kDnamseHlr	hfpnCcFI		
SEQ ID NO:23	hiap2-2	eearFlTYhm	WP.lflsps	eLARAGFYI	GpgDrVaCfa	CggklknWep	kDdamseHrr	hfpnCcFI		
SEQ ID NO:24	m-xiap-3	yearRivTFgt	Wiysv..nke	qLARAGFYal	GegDkVkcFh	CgggltdWkp	sEdpwdqHak	cyPgCkYl		
SEQ ID NO:25	xiap-3	yearRifTFgt	Wiysv..nke	qLARAGFYal	GegDkVkcFh	CgggltdWkp	sEdpweqHak	wyPgCkYl		
SEQ ID NO:26	hiap1-3	haaRfkTFfn	WPssvlvnpe	qLASAGFYV	GnsDdVkcFC	CdggllrcWes	gDdpwvqHak	wfPrC Yl		
SEQ ID NO:27	hiap2-3	haaRmrTFmy	WPssvpvqpe	qLASAGFYV	GnsDdVkcFC	CdggllrcWes	gDdpwveHak	wfPrCeFl		
SEQ ID NO:28	Op_iap-2	eaarLrTFae	WPrglkqrpe	eLAeAGFFYt	GqgDktrCFc	CdggllkdWep	dDapwqqHar	wydrCeYV		
SEQ ID NO:29	Cp_iap-2	eaarVksFhn	WPrckmqrpe	qMAdAGFFYt	GygDntkCFY	CdggllkdWep	eDvpweqHvr	widrCaYV		
SEQ ID NO:30	diap-3	vdarLrTFtd	WPisniqpas	aLAqAGLYYq	kigDqVrCFh	Cniglrswqk	eDepwieHak	wspkCqFV		
SEQ ID NO:31	diap-1	esvRLaTFge	WPlnapvsae	dlvanGFF..	GtwmeaeCdf	ChvridrWey	gDlvaerHrr	sspiCsmv		
SEQ ID NO:2	Consensus	---RL-TF--	WP-----	-LA-AGFY-	G--D-V-CF-	C-----W--	-D-----H--	--P-C-FV		

SEQ ID NO:12	1	cp-iap	50
SEQ ID NO:13	...	diap	...
SEQ ID NO:10	...	m-xiap	...
SEQ ID NO:4	...	xiap	...
SEQ ID NO:6	...	hiap1	...
SEQ ID NO:8	...	hiap2	...
SEQ ID NO:44	...	consensus	...
BIR 1			
51	100		
cp-iap	...	...	...
diap	...	...	...
m-xiap	...	...	...
xiap	...	...	...
hiap1	...	...	...
hiap2	...	...	...
consensus	...	...	...
BIR 1			
101	150		
cp-iap	...	...	...
diap	...	...	...
m-xiap	...	...	...
xiap	...	...	...
hiap1	...	...	...
hiap2	...	...	...
consensus	...	...	...

Fig. 8A

151	cp-iap	.....	.....mSD	lrl.....	EEvRLnTF	200
	diap	esDnegnsVv	dspscscpD	lll.....	EEanRLvTF	ekWPv.sfls
	m-xiap	ppEthadyll	rtgqvDiSD	tiyprnp.am	csEEARLksF	kdWpn.pnit
	xiap	psEthadyll	rtgqvDiSD	tiyprnp.am	ycEEARLksF	qnWpdyahLt
	hiap1	anq.....	.....EfSa	lmrssypcpM	nnEnARLlTF	qnWpdyahLt
	hiap2	avE.....	.....DiSs	srtnpysyam	stEEARFlTY	qtWP.ltfIs
	consensus	--E-----	-----D-SD	-----M	EEARL-TF	hmWP.ltfIs
						--WP-----L-
201	cp-iap	PetMAknGFY	YlGrSDeVrC	afCkveImrW	kegEdpaadH	250
	diap	PqaLakAGFY	YlnrldhVkc	vwCnGviakW	EkndnAfeEH	kkwaPqCPFV
	m-xiap	PrELASAGLY	YtGadDqVqC	FcCGGKLkNW	EPcDrAwSEH	kRfFPqCPrV
	xiap	PrELASAGLY	YtGigDqVqC	FcCGGKLkNW	EPcDrAwSEH	rRHFPnCfFV
	hiap1	PtDLARAGFY	YiGpgDrVaC	FaCGGKLsNW	EPkDnAmSEH	rRHFPnCfFV
	hiap2	PsELARAGFY	YiGpgDrVaC	FaCGGKLsNW	EPkDdAmSEH	lRHFPkCPFI
	consensus	P-ELA-AGFY	Y-G--D-V-C	F-CGGKL-NW	EP-D-A-SEH	rRHFPnCpFl
						-RHFP-CPFV
251	cp-iap	kgidvcgsiv	ttnniqnttt	hdtiigPahP	kyAheaARvk	300
	diap	qmgplie.fa	tgknldelgi	qpttl.Plrp	kyAcvdARlr	sFhnWPrCmk
	m-xiap	lgrnvnvrse	s.gvssdrnF	pnstnsPrNP	aMAeyeARiv	TftdWPiSnI
	xiap	lgrnlmrse	sdavssdrnF	pnstnlPrNP	sMAdyeARif	TFgtWiys..
	hiap1	.....	enqlqdtSry	tvS.....Nl	smQtthaARfk	TFgtWiys..
	hiap2	.....	ensl.etlrf	sis.....Nl	smQtthaARmr	TFfnWPSSvl
	consensus	-----	-----F	--S---p-NP	-MA---AR--	TFmyWPSSvp
						TF--WP-S--

Fig. 8B

BIR 3		350
cp-iap	qrpeQMaDAG FFYtGyGDnt KCFyCdGGLk dWepeDvPWe	QHvrWFdrCa
diap	qpasaLaqAG LYyqkiGdqv rCFhCniGLr swqkeDEPwf	eHAKWspkCq
m-xiap	VnkeQLaRAG FYalGeGDkV KCFhCgGGLt dwkpsEDPwD	QHAKcYPgCk
xiap	VnkeQLaRAG FYalGeGDkV KCFhCgGGLt dwkpsEDPwD	QHAKWYPgCk
hiap1	VnpEQLaSAG FYYvGnsDdV KCFcCdGGLr cwesgDDPwV	QHAKWFFPrCe
hiap2	VqpEQLaSAG FYYvGRSDdV KCFgCdGGLr cwesgDDPwV	eHAKWFFPrCe
consensus	V--EQLA-AG FYY-G-GD-V KCF-C-GGL-	-W---DDPW- QHAKWFFP-C-
		351
cp-iap	YvqlvKGrDY VqkVit.....	.....e.....
diap	FvllakGpay Vsevlattaa nassqpaTap aptlq.....	.....Ppltk
m-xiap	YlldeKGQeY InnIhlthp. LeEsLgrTae kt.....	.....Psltr
xiap	YlldegKGQeY InnIhlthp. LeEcLvrTte kt.....	.....ihlePgEdh
hiap1	YlirirKGQeY IrqVqasyph LLEqLlTsD spgdenaess	.....ihfgPgess
hiap2	FlirrmKGQeF VdeIggryph LLEqLlTsD ttgeenadpp	.....p----
consensus	Yl---KGQeY ----- L-E-L--T--	-----p----
		400
		401
cp-iap	..acVLpge.	.....
diap	..adVLmdea pakeAltLGi dggvVrnaiq rKlLssGcaF	stldeLlhDi
m-xiap	kiDdtifgnP mVqeAirMGF sfkdLkktme eKIqtsGssY	lslevLlaDL
xiap	riDdtifgnP mVqeAirMGF sfkdIKkime eKIqisGsnY	kslevLVaDL
hiap1	seDaIMmntP vInaAveMGF srsLVKgtvq rKIlatGenY	rlvndLVlDL
hiap2	seDaVMmntP vKsAleMGF nrdLVKgtvI sKIlttGenY	ktvndiVsAl
consensus	--D-V----P -V--A--MGF -----VK----	-KI---G--Y -----LV-DL
		450

Fig. 8C

```

451                                     500
cp-iap                               .....
diap   fddagagaal Evreppe.....
m-xiap vsAqkDnted E.....
xiap   vnAqkDsmqD E.....
hiap1  lnAedEireE Ererateeke sndlllrkn rmalfqhltc vipildsilt
hiap2  lnAedEkreE Ekekqaema sddslirkn rmalfqqltc vipildnllk
consensus --A----- E-----

501                                     550
cp-iap                               .....
diap   ..... ..nttvstaa pvsepipe.. .....
m-xiap ..... ..psapfie pcgattskaa svpipvads i pakpqaeeav
xiap   ..... ..ssQtsL Q.....
hiap1  ..... ..ssQtsL Q.....
hiap2  agineqehd vikqktQtsL Qarelidtil vkgniaatvf rnslqaeav
consensus anvinkqehd iikqktQipl Qarelidtiw vkgnaaanif knclkeidst
          -----Q--L Q-----

```

Fig. 8D

		Ring Zinc Finger	
551			600
cp-iap	...tki...	Ekepq	veDskLCKIC yveEciVCFV
diap	sniskitdei	nlSlEEEnRq	LkDarLCKVC LDeEVgVVF1
m-xiap	.....	diStEEQLRR	LqEEkLskIC MDrnIaIVFf
xiap	.....	eiStEEQLRR	LqEEkLCKIC MDrnIaIVFV
hiap1	iyehlfvqqd	ikyiptedvs	dlpVEEQLRR LpEErtCKVC MDkEVsIVFI
hiap2	lyknlfvdkn	mkyiptedvs	glSlEEQLRR LqEErtCKVC MDkEVsVVF1
consensus	-----	---S-EEQLRR	L-EE-LCK-C MD-EV--VF-
601			635
cp-iap	PCGHVvCaK	CALSVdKCPM	QRkIVtSVlk vVFS.
diap	PCGHLatCnq	CAPSVanCPM	QRadIkqfvr tFLS*
m-xiap	PCGHLatCkq	CAeaVdKCPM	CytVItfngk iFMS*
xiap	PCGHLVtCkq	CAeaVdKCPM	CytVItfkqk iFMS*
hiap1	PCGHLVvCkd	CAPslrKCPi	QRstIkgtvr tFLS*
hiap2	PCGHLVvCqe	CAPslrKCPi	QRgIIkgtvr tFLS.
consensus	PCGHLV-C--	CA-SV-KCPM	QR--I----- -FLS-

Fig. 8E

# Alignment of RZF (Ring Zinc Finger) Domains

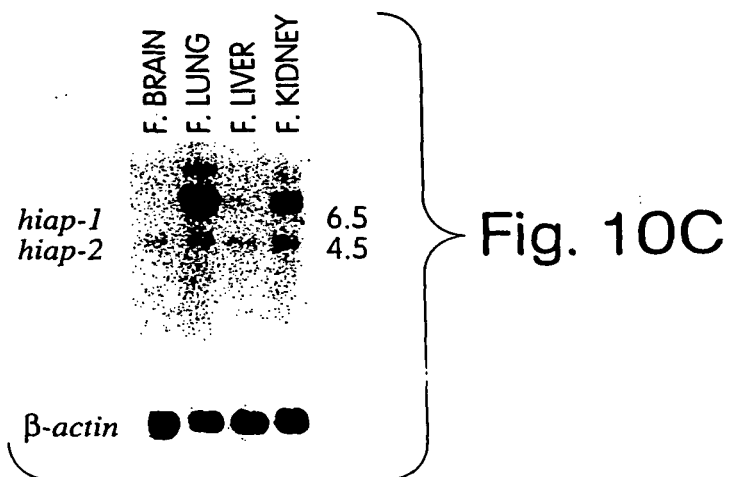
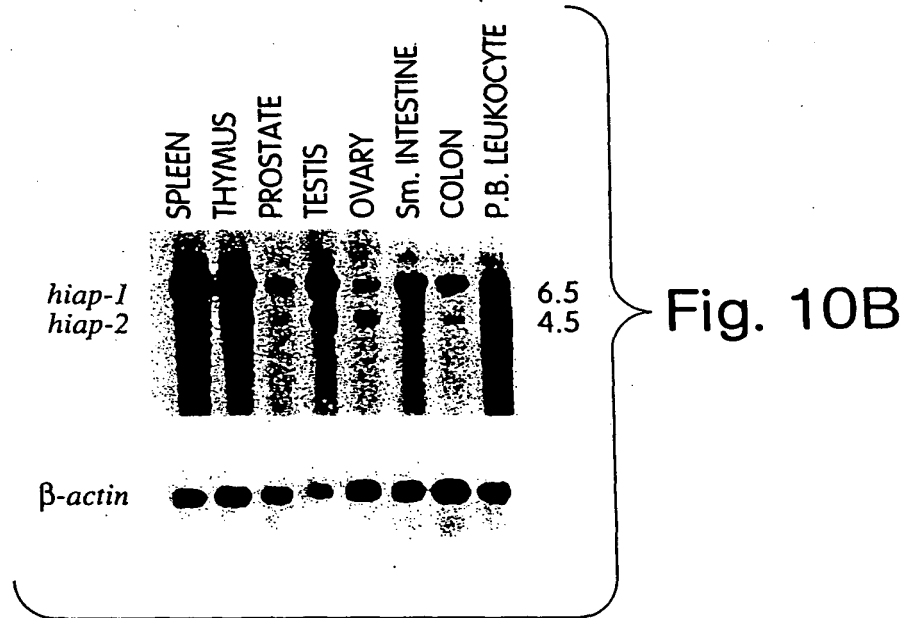
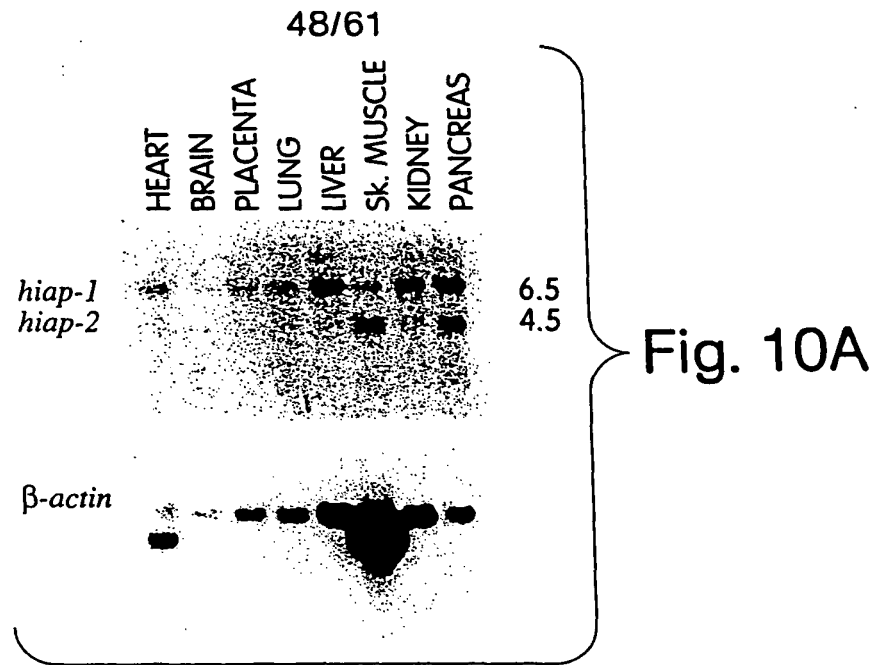
<b>Baculovirus</b>	
Cp_iap	Cydia pomonella
Op_iap	Orgyia pseudotsugata
<b>Human</b>	
xiap	IAP on X chromosome
hiap1, hiap2	two different human IAP genes
<b>Mouse</b>	
m-xiap	mouse homologue of human xiap gene
<b>Insect</b>	
diap	Drosophila IAP gene, not clearly a homologue of xiap or hiap

## note on consensus:

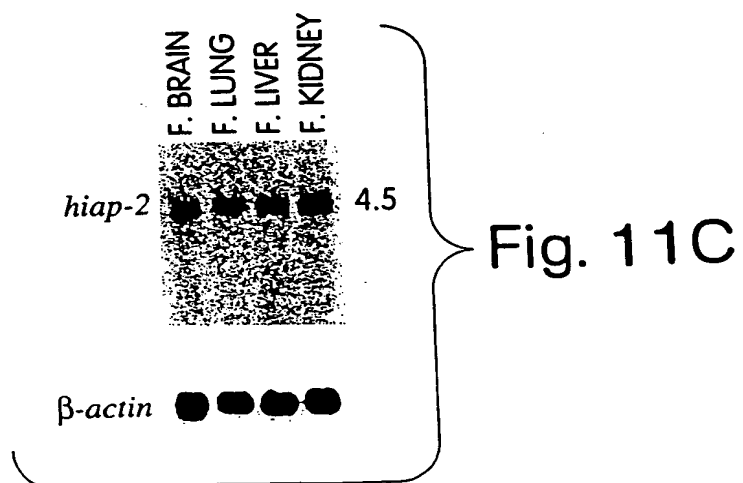
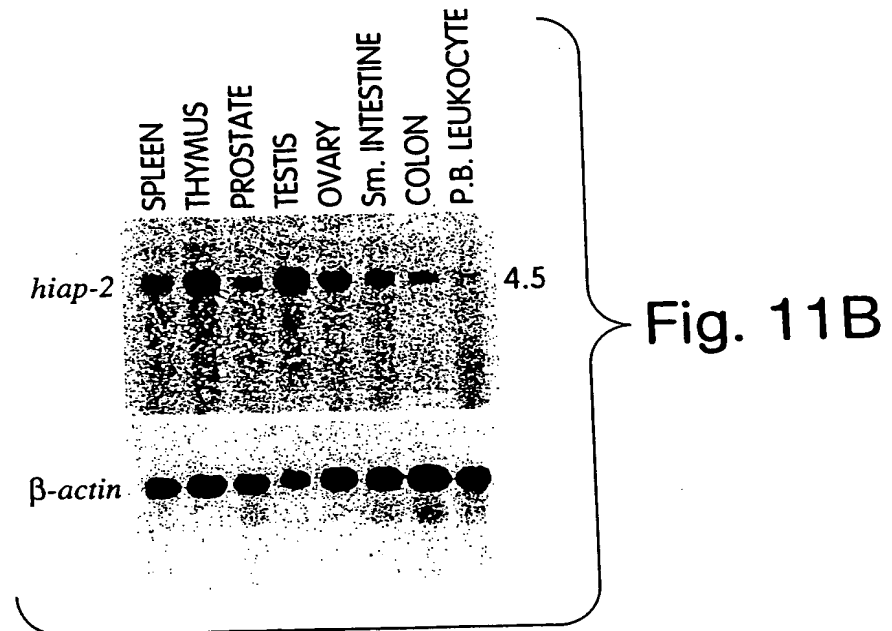
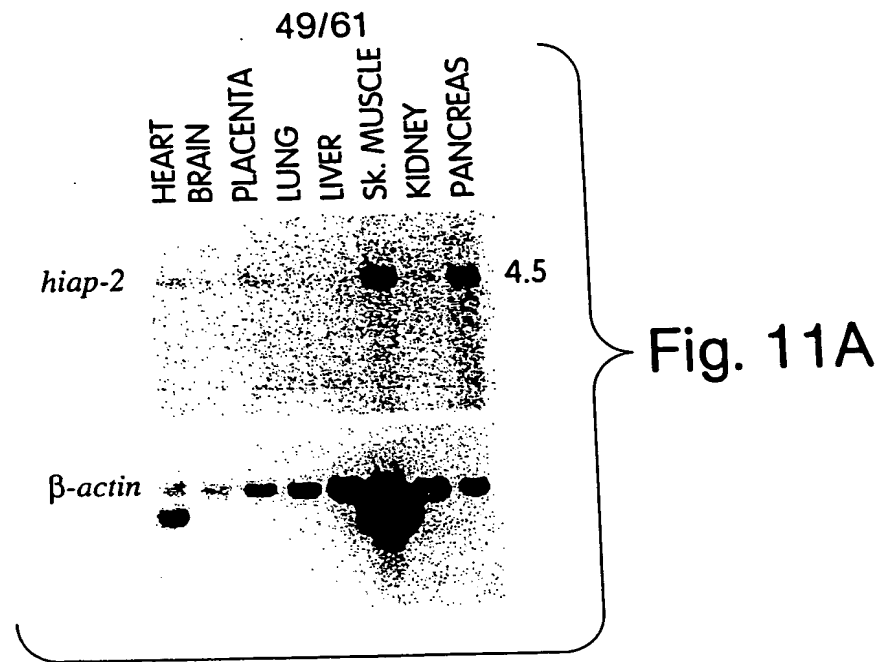
The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

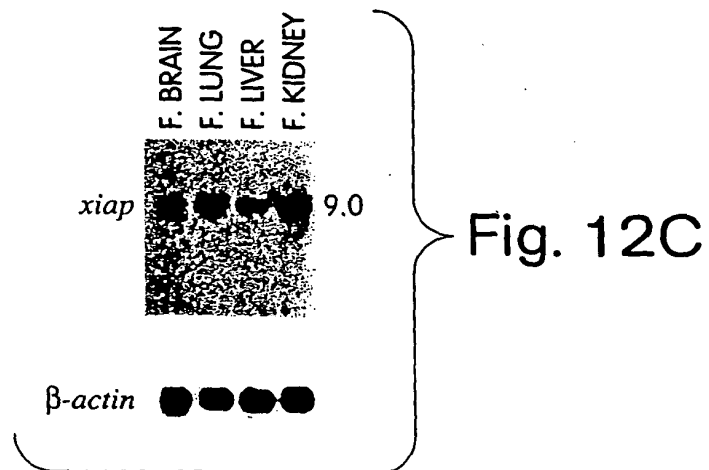
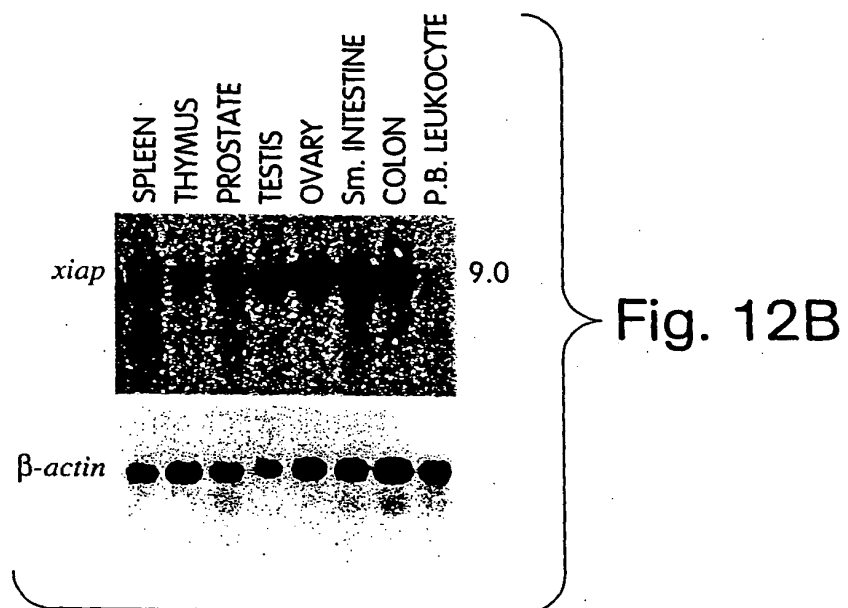
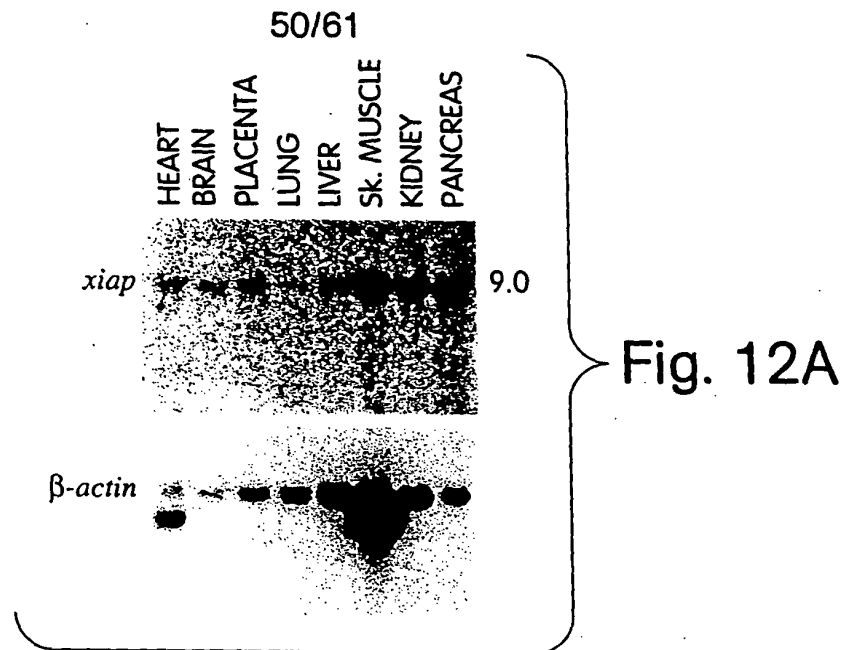
SEQ ID NO:32	hiap2	1	EqlrrlqEer	tCKVCMdkev	sVvFiPCGH1	vVCqeCApel	rkCPiC	46
SEQ ID NO:33	hiap1		EqlrrlpEer	tCKVCMdkev	sIVFiPCGH1	w CkdCAPs1	rkCPiC	
SEQ ID NO:34	m-xiap		EqlrrlqEek	lSKICMdrni	aIVFfPCGH1	atCkqCAeav	dkCPmC	
SEQ ID NO:35	xiap		EqlrrlqEek	lCKICMdrni	aIVFvPCGH1	vtCkqCAeav	dkCPmC	
SEQ ID NO:36	diap		EenrqlkDar	lCKVCLdeev	gVvFlPCGH1	atCnqCApev	anCPmC	
SEQ ID NO:37	Cp_iap		EkepgveDsk	lCKICyveec	iVcFvPCGHv	vaCakCALsv	dkCPmC	
SEQ ID NO:38	Op_iap		aveaevaDdr	lCKIClgack	tVcFvPCGHv	vaCgkCAagv	ttCPvC	
SEQ ID NO:1	consensus		E-----E--	-CKICM----	-V-F-PCGH-	--C--CA---	--CP-C	

Fig. 9









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S: STANDARDS		INCUBATION: OVERNIGHT											
		Hg			CEM-CM <sub>3</sub>			GT/CEM			JKT		
HIV		-	-	+	-	-	+	-	-	+	-	-	+
PHA/PMA		-	+	-	-	+	-	-	+	-	-	+	-
S		+	-	-	+	-	-	+	-	-	+	-	-

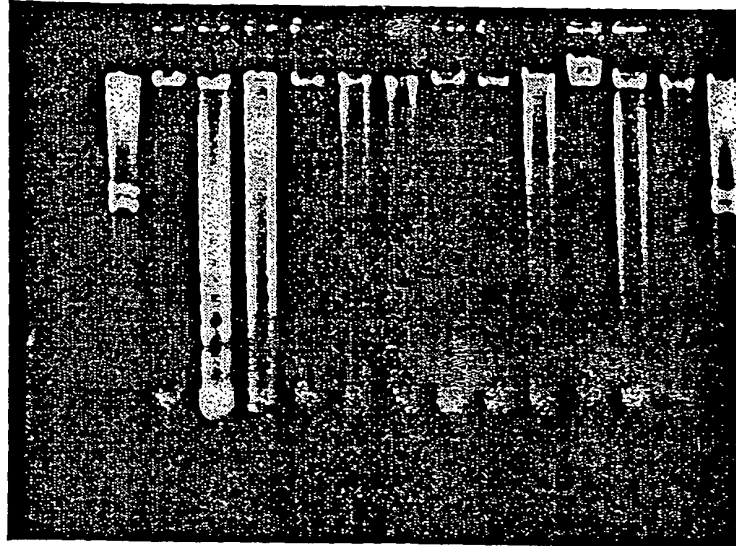


Fig. 13A

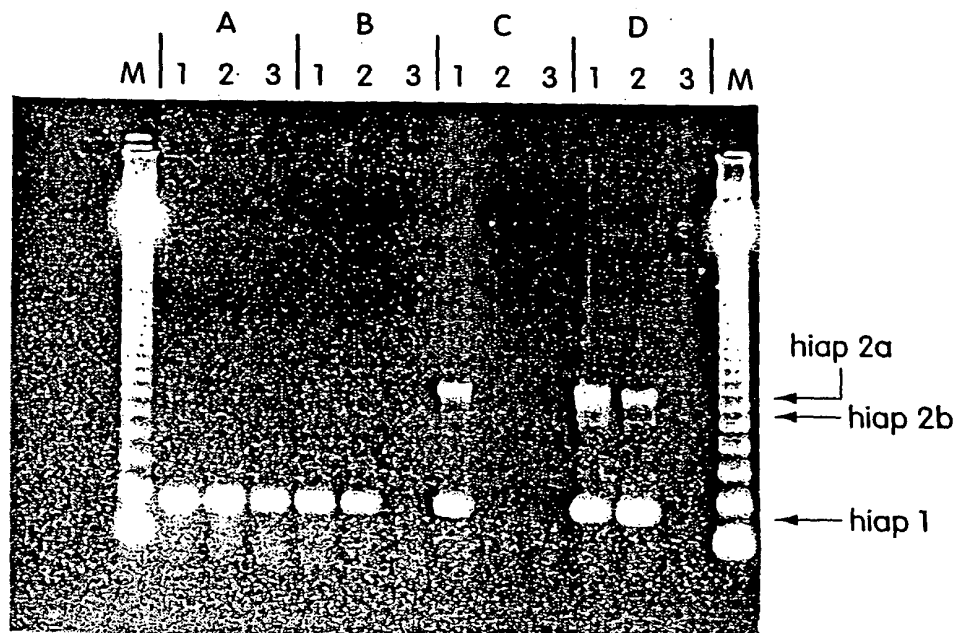


Fig. 13B

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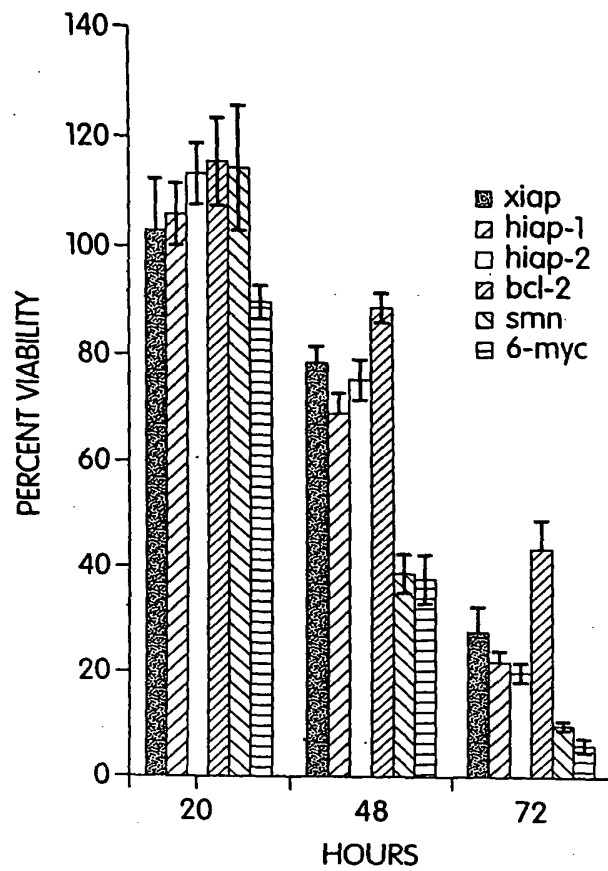


Fig. 14A

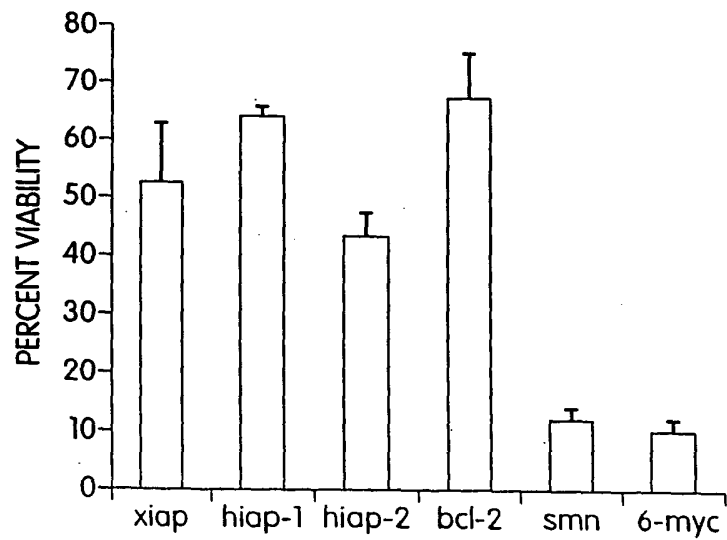


Fig. 14B

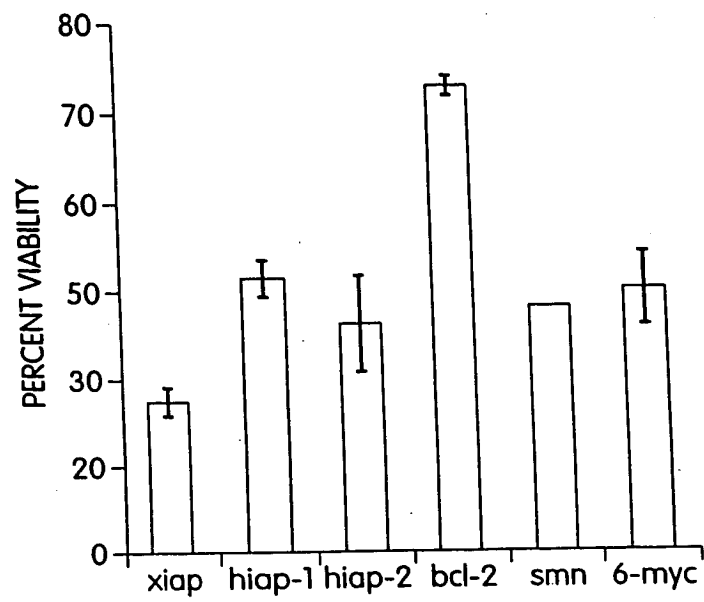


Fig. 14C

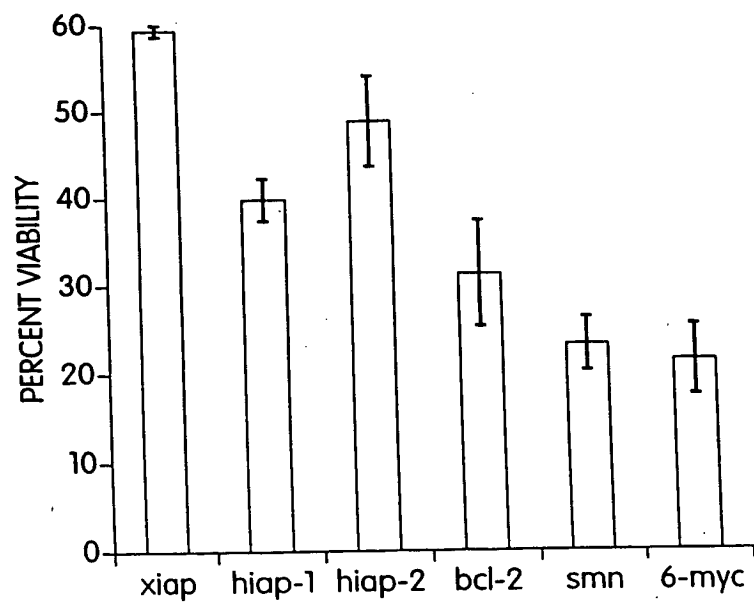


Fig. 14D

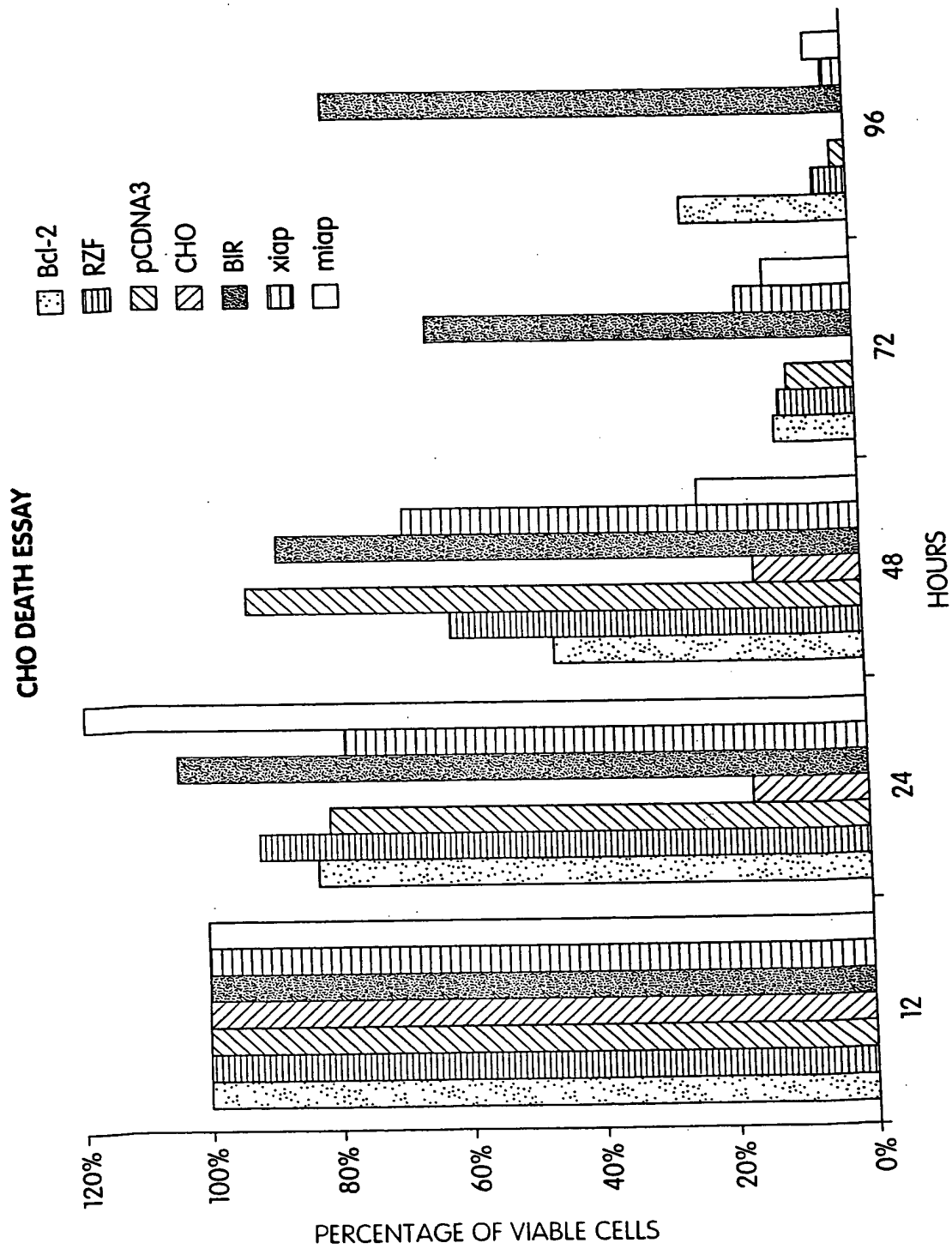
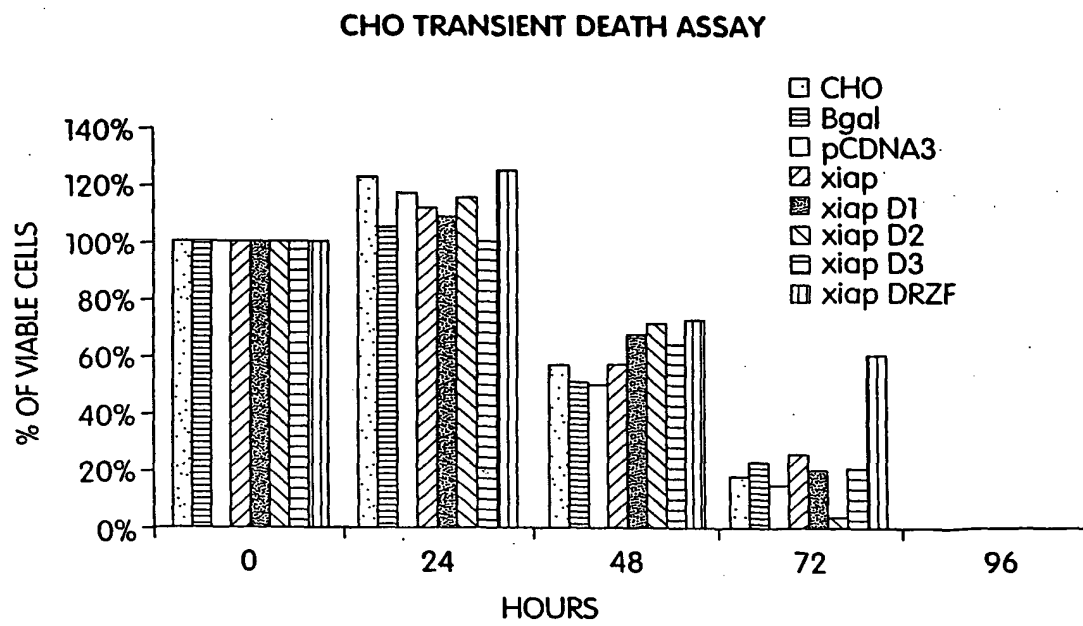


Fig. 15A

**Fig. 15B**

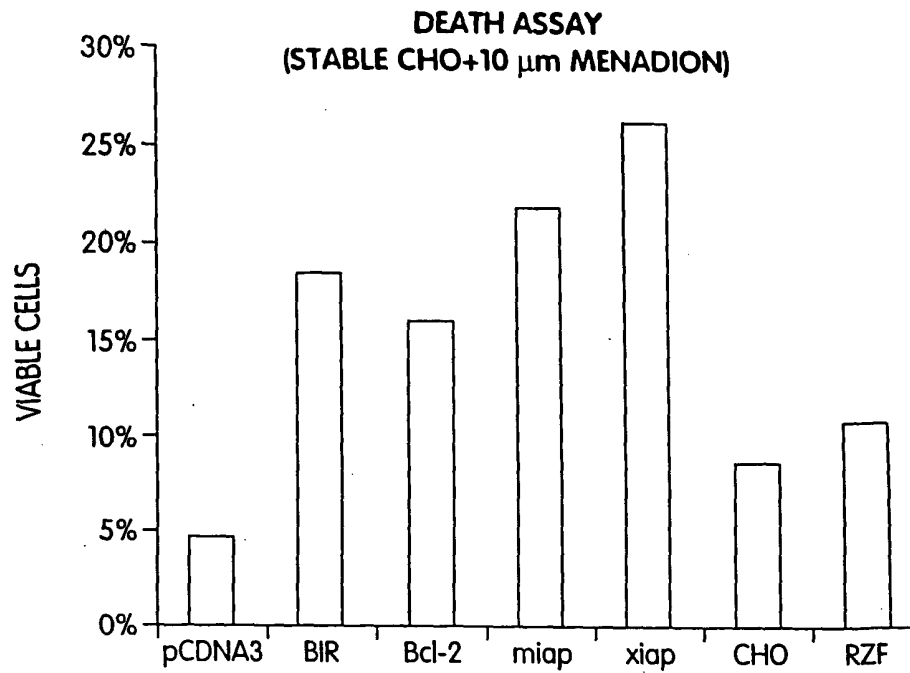


Fig. 16A

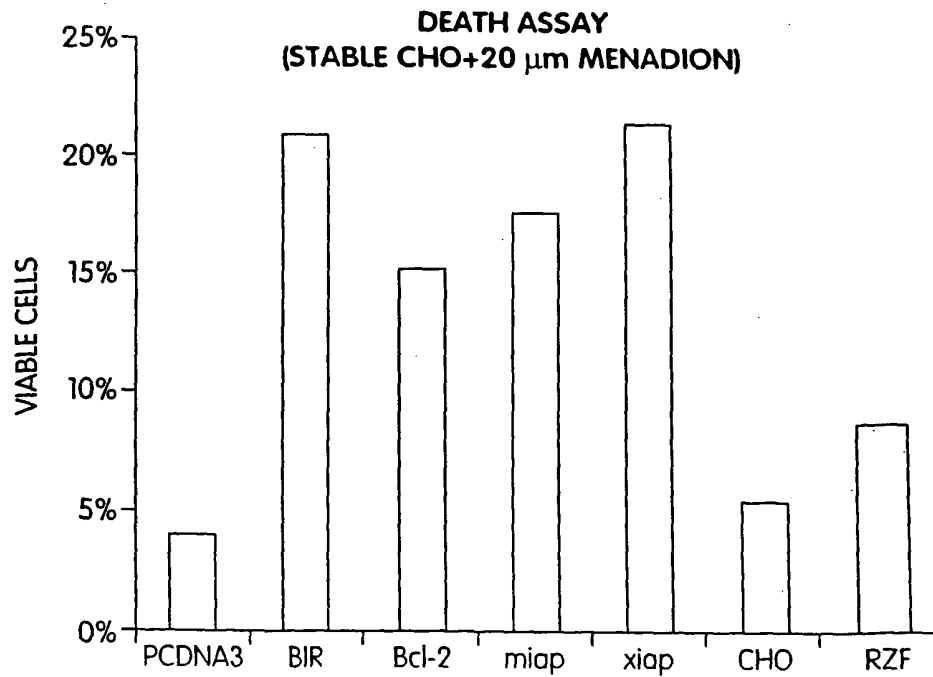


Fig. 16B



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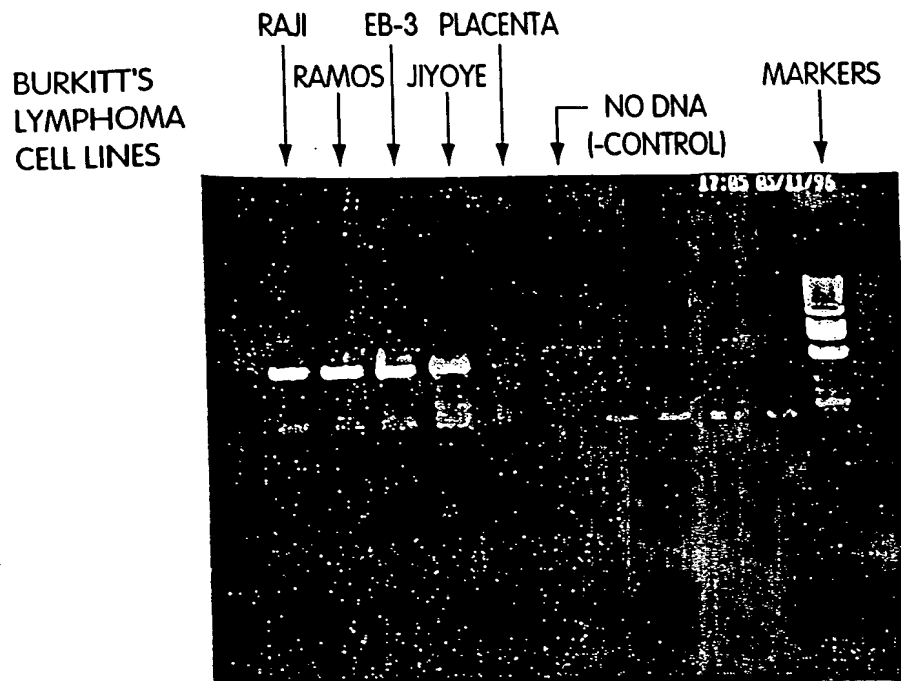


Fig. 17

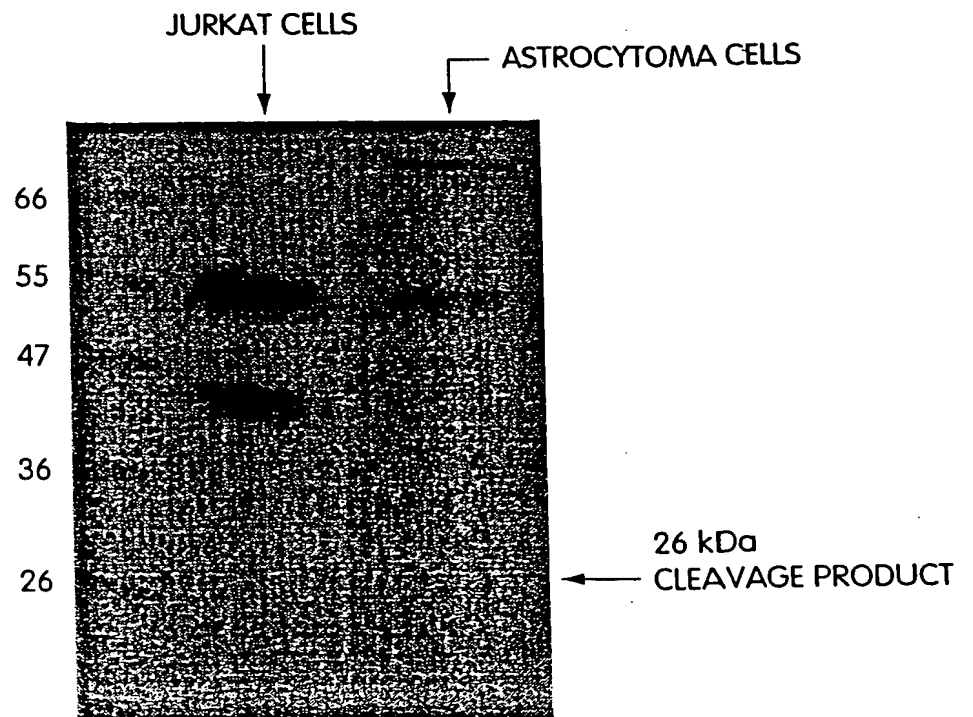


Fig. 18

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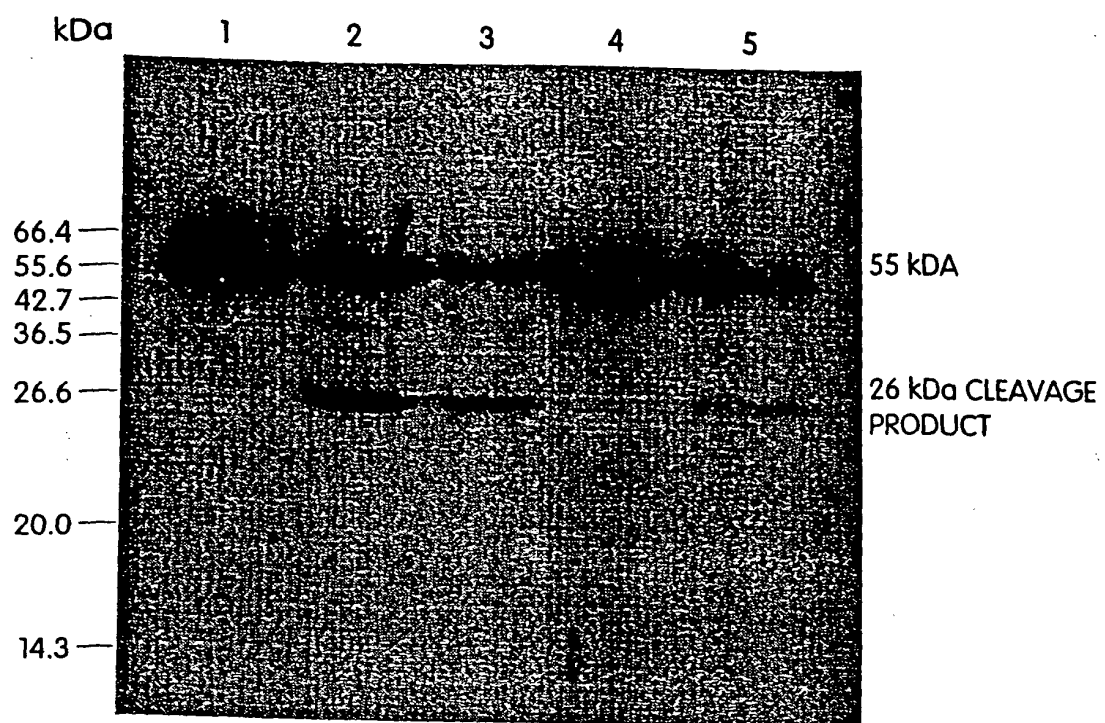


Fig. 19

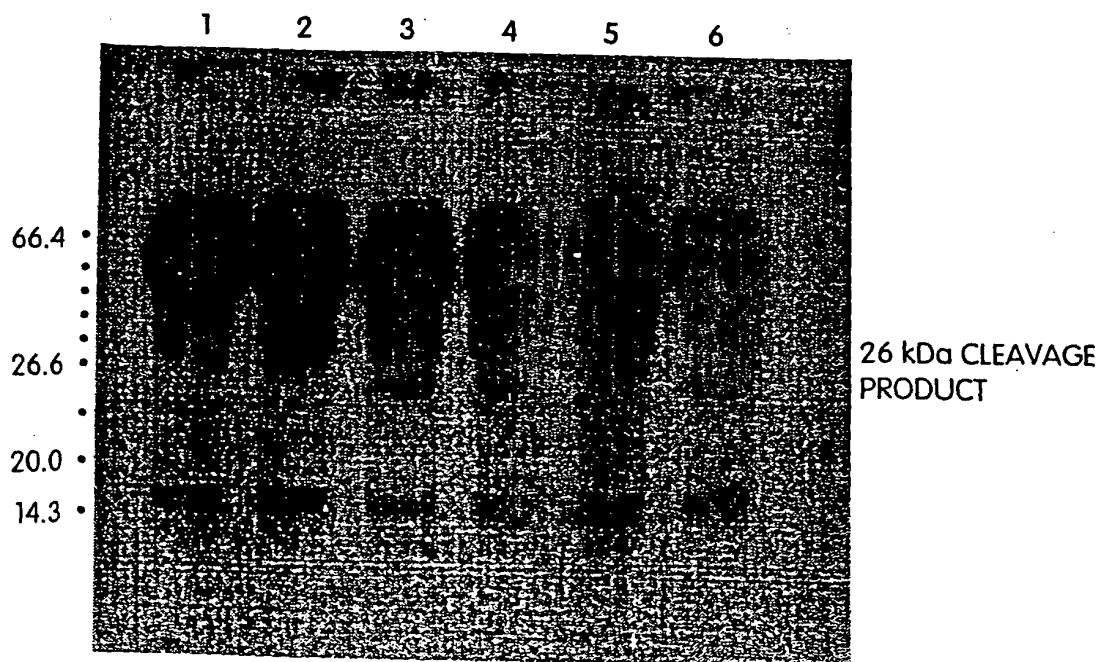


Fig. 20

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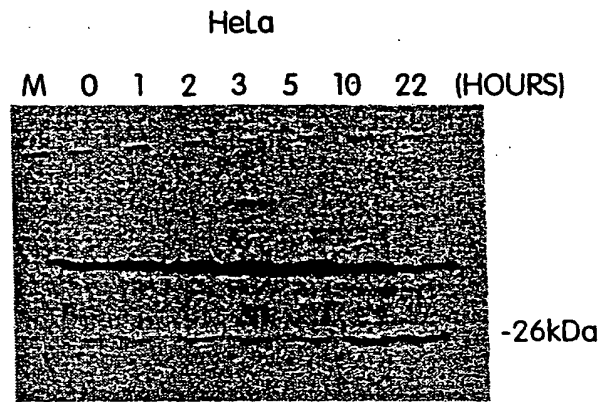


Fig. 21A

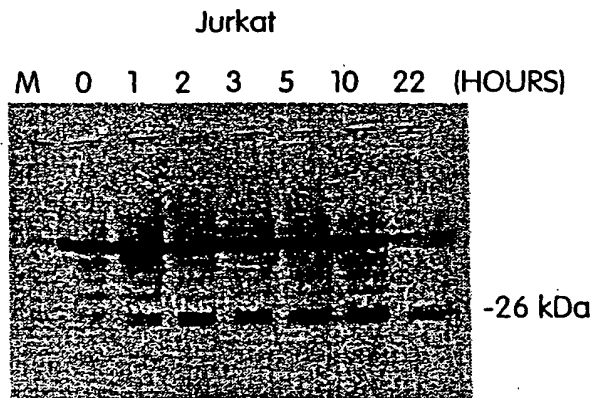


Fig. 21B

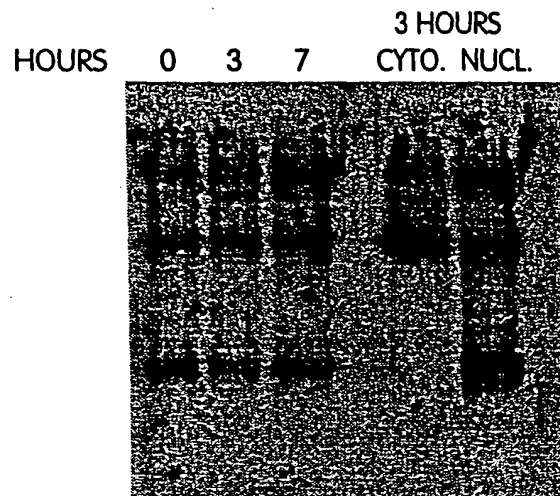


Fig. 22A

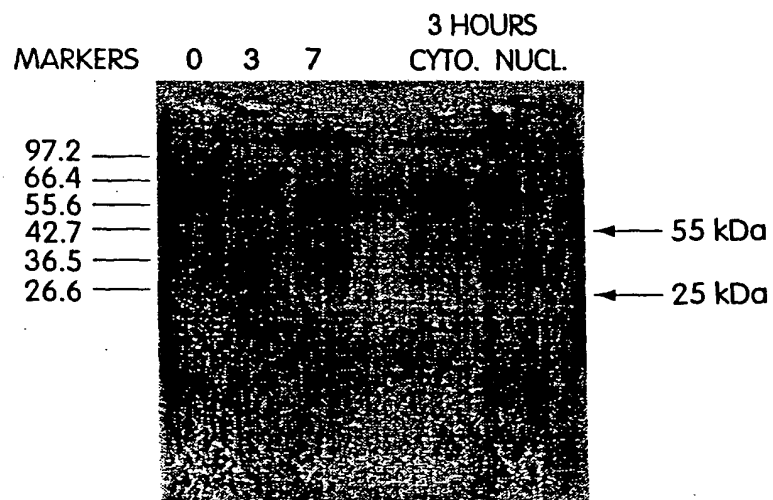


Fig. 22B

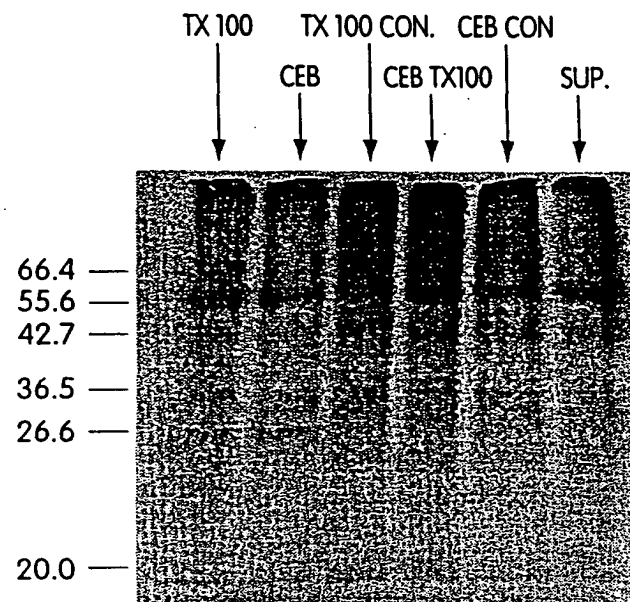


Fig. 23